

## SEQUENCE LISTING

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- <120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350  
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- <150> PCT/US00/04414  
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- <150> US 60/143,048  
<151> 1999-07-07
- <150> US 60/145,698  
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- <150> US 60/146,222  
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- <150> PCT/US99/20594  
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- <150> PCT/US99/20944  
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<210> 2

<211> 353

<212> PRT

<213> Homo sapiens

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```

```

Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
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```

```

Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
    50                      55                      60

```

```

Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
    65                      70                      75                      80

```

```

Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
                85                      90                      95

```

```

Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
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```

Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
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Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
    130                      135                      140

```

Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg  
145 150 155 160

Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu  
165 170 175

Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr  
180 185 190

His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly  
195 200 205

Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp  
210 215 220

Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro  
225 230 235 240

Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys  
245 250 255

Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly  
260 265 270

Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys  
275 280 285

Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys  
290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro  
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Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala  
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<211> 2206

<212> DNA

<213> Homo sapiens

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aacagccctg gctgagggag ctgcagcgca gcagagtatc tgacggcgcc aggttgcgta 180  
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<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

<400> 4

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```

Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
      20              25              30

```

```

Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
      35              40              45

```

```

Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
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```

```

Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile

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Ile	Met	Ala	Asp	Pro	Thr	Val	Asn	Val	Pro	Leu	Leu	Gly	Thr	Val	Pro
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His	Lys	Ala	Ser	Val	Val	Gln	Val	Gly	Phe	Pro	Cys	Leu	Gly	Lys	Gln
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225					230					235					240
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290						295					300				
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305					310					315					320
His	Glu	Pro	Asn	Lys	Cys	Gln	Cys	Gln	Glu	Gly	Trp	His	Gly	Arg	His
				325					330					335	
Cys	Asn	Lys	Arg	Tyr	Glu	Ala	Ser	Leu	Ile	His	Ala	Leu	Arg	Pro	Ala
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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 <223> Description of Artificial Sequence: Synthetic  
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<400> 7  
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<220>  
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 oligonucleotide probe

<400> 9  
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<210> 10  
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 <213> Artificial Sequence

<220>  
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 oligonucleotide probe

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<210> 12

<211> 164

<212> PRT

<213> Homo sapiens

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Met Trp Arg Cys Pro Leu Gly Leu Leu Leu Leu Leu Pro Leu Ala Gly
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```

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His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
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```

```

Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
      35                      40                      45

```

```

Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
      50                      55                      60

```

```

Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
      65                      70                      75                      80

```

```

Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
          85                      90                      95

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```

Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
      100                      105                      110

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```

Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
      115                      120                      125

```

```

Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
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Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
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His Asp Pro Gly

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 <213> Homo sapiens

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 oligonucleotide probe

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<210> 15

<211> 22

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oligonucleotide probe

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<210> 16

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 17

<211> 960

<212> DNA

<213> Homo sapiens

<400> 17

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<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

&lt;400&gt; 18

Met Thr His Arg Thr Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val  
 1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu  
 20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp  
 35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly  
 50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp  
 65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met  
 85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser  
 100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Asp Thr Asp Pro Pro Ala  
 115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe  
 130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe  
 145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser  
 165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln  
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&lt;210&gt; 19

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 19

tgctgtgcta ctctgcaaa gcc

24

&lt;210&gt; 20

&lt;211&gt; 24

&lt;212&gt; DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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gaccgaccag ctgagcaggc ggcagatccg cgagtaccaa ctctacagca ggaccagtgg 180
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<210> 23

<211> 205

<212> PRT

<213> Homo sapiens

&lt;400&gt; 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu  
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Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met  
 20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser  
 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala  
 50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp  
 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr  
 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys  
 100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr  
 115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg  
 130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu  
 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn  
 165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr  
 180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr  
 195 200 205

&lt;210&gt; 24

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

&lt;400&gt; 24

cagtacgtga gggaccaggg cgccatga

28

&lt;210&gt; 25

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 25  
 ccggtgacct gcacgtgctt gccca 24

<210> 26  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<220>  
 <221> modified\_base  
 <222> (21)  
 <223> a, t, c or g

<400> 26  
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<210> 27  
 <211> 2479  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
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 cttttttcct gaagtcttg cttatcattt ccctggggct ctactcacag gtgtccaaac 360  
 tcttgacctg ccctagtgtg tgccgctgcg acaggaactt tgtctactgt aatgagcgaa 420  
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 atctgatcag gctctatttg caggacaacc agataaacca cattcctttg acagccttct 1080  
 caaatctgcg taagctggaa cggctggata tatccaacaa ccaactgcgg atgctgactc 1140

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```

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

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Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
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```

```

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
      20                      25                      30

```

```

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
      35                      40                      45

```

```

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
      50                      55                      60

```

```

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
      65                      70                      75                      80

```

```

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
      85                      90                      95

```

```

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
      100                      105                      110

```

```

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
      115                      120                      125

```

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser  
 130 135 140  
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser  
 145 150 155 160  
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val  
 165 170 175  
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile  
 180 185 190  
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg  
 195 200 205  
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly  
 210 215 220  
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn  
 225 230 235 240  
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg  
 245 250 255  
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe  
 260 265 270  
 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu  
 275 280 285  
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln  
 290 295 300  
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp  
 305 310 315 320  
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly  
 325 330 335  
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu  
 340 345 350  
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro  
 355 360 365  
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro  
 370 375 380  
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro  
 385 390 395 400  
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg

				405						410					415
Val	Thr	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Gln	Leu	Ser	Ile	His	Phe	Val
			420						425				430		
Asn	Asp	Thr	Ser	Ile	Gln	Val	Ser	Trp	Leu	Ser	Leu	Phe	Thr	Val	Met
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Ala	Tyr	Lys	Leu	Thr	Trp	Val	Lys	Met	Gly	His	Ser	Leu	Val	Gly	Gly
	450					455					460				
Ile	Val	Gln	Glu	Arg	Ile	Val	Ser	Gly	Glu	Lys	Gln	His	Leu	Ser	Leu
465					470					475					480
Val	Asn	Leu	Glu	Pro	Arg	Ser	Thr	Tyr	Arg	Ile	Cys	Leu	Val	Pro	Leu
				485					490					495	
Asp	Ala	Phe	Asn	Tyr	Arg	Ala	Val	Glu	Asp	Thr	Ile	Cys	Ser	Glu	Ala
			500					505					510		
Thr	Thr	His	Ala	Ser	Tyr	Leu	Asn	Asn	Gly	Ser	Asn	Thr	Ala	Ser	Ser
		515					520					525			
His	Glu	Gln	Thr	Thr	Ser	His	Ser	Met	Gly	Ser	Pro	Phe	Leu	Leu	Ala
	530					535					540				
Gly	Leu	Ile	Gly	Gly	Ala	Val	Ile	Phe	Val	Leu	Val	Val	Leu	Leu	Ser
545					550					555					560
Val	Phe	Cys	Trp	His	Met	His	Lys	Lys	Gly	Arg	Tyr	Thr	Ser	Gln	Lys
				565					570					575	
Trp	Lys	Tyr	Asn	Arg	Gly	Arg	Arg	Lys	Asp	Asp	Tyr	Cys	Glu	Ala	Gly
			580					585					590		
Thr	Lys	Lys	Asp	Asn	Ser	Ile	Leu	Glu	Met	Thr	Glu	Thr	Ser	Phe	Gln
		595					600					605			
Ile	Val	Ser	Leu	Asn	Asn	Asp	Gln	Leu	Leu	Lys	Gly	Asp	Phe	Arg	Leu
	610					615					620				
Gln	Pro	Ile	Tyr	Thr	Pro	Asn	Gly	Gly	Ile	Asn	Tyr	Thr	Asp	Cys	His
625					630					635				640	
Ile	Pro	Asn	Asn	Met	Arg	Tyr	Cys	Asn	Ser	Ser	Val	Pro	Asp	Leu	Glu
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His	Cys	His	Thr												
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<210> 29  
 <211> 21  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 29

cggtctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

<213> Homo sapiens

<400> 33

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gaggaagacc cgggtggctg cggccctgcc tgccttccca ggcgcggcg gctgcagcct 180  
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ctgtagaaca ctggccatag gaaatgctgt tttttgtac tggactttac cttgatatat 3360
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<210> 34

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
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Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
      35              40              45

Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
      50              55              60

Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
      65              70              75              80

Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
      85              90              95

Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
      100             105             110

Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
      115             120             125

His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
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Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
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Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
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Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
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Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
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Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
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Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His

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225					230				235				240			
Met	Cys	Ser	Thr	Leu	Glu	His	Asn	Cys	Ala	His	Phe	Cys	Ile	Asn	Ile	
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Pro	Gly	Ser	Tyr	Val	Cys	Arg	Cys	Lys	Gln	Gly	Tyr	Ile	Leu	Asn	Ser	
				260				265				270				
Asp	Gln	Thr	Thr	Cys	Arg	Ile	Gln	Asp	Leu	Cys	Ala	Met	Glu	Asp	His	
				275				280				285				
Asn	Cys	Glu	Gln	Leu	Cys	Val	Asn	Val	Pro	Gly	Ser	Phe	Val	Cys	Gln	
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Cys	Tyr	Ser	Gly	Tyr	Ala	Leu	Ala	Glu	Asp	Gly	Lys	Arg	Cys	Val	Ala	
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Val	Asp	Tyr	Cys	Ala	Ser	Glu	Asn	His	Gly	Cys	Glu	His	Glu	Cys	Val	
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Asn	Pro	Asp	Glu	Lys	Thr	Cys	Thr	Arg	Ile	Asn	Tyr	Cys	Ala	Leu	Asn	
				355				360				365				
Lys	Pro	Gly	Cys	Glu	His	Glu	Cys	Val	Asn	Met	Glu	Glu	Ser	Tyr	Tyr	
				370				375				380				
Cys	Arg	Cys	His	Arg	Gly	Tyr	Thr	Leu	Asp	Pro	Asn	Gly	Lys	Thr	Cys	
385					390				395				400			
Ser	Arg	Val	Asp	His	Cys	Ala	Gln	Gln	Asp	His	Gly	Cys	Glu	Gln	Leu	
				405				410				415				
Cys	Leu	Asn	Thr	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Ser	Glu	Gly	Phe	
				420				425				430				
Leu	Ile	Asn	Glu	Asp	Leu	Lys	Thr	Cys	Ser	Arg	Val	Asp	Tyr	Cys	Leu	
				435				440				445				
Leu	Ser	Asp	His	Gly	Cys	Glu	Tyr	Ser	Cys	Val	Asn	Met	Asp	Arg	Ser	
				450				455				460				
Phe	Ala	Cys	Gln	Cys	Pro	Glu	Gly	His	Val	Leu	Arg	Ser	Asp	Gly	Lys	
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Thr	Cys	Ala	Lys	Leu	Asp	Ser	Cys	Ala	Leu	Gly	Asp	His	Gly	Cys	Glu	
				485				490				495				
His	Ser	Cys	Val	Ser	Ser	Glu	Asp	Ser	Phe	Val	Cys	Gln	Cys	Phe	Glu	
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Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val  
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Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln  
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 Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu  
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 Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp  
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 Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser  
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 Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

&lt;210&gt; 38

&lt;211&gt; 1813

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 38

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&lt;210&gt; 39

&lt;211&gt; 390

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 39

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Leu	His	Leu	Pro	Ala	Asn	Arg	Leu	Gln	Ala	Val	Glu	Gly	Gly	Glu	Val	
			35				40						45			
Val	Leu	Pro	Ala	Trp	Tyr	Thr	Leu	His	Gly	Glu	Val	Ser	Ser	Ser	Gln	
			50				55						60			
Pro	Trp	Glu	Val	Pro	Phe	Val	Met	Trp	Phe	Phe	Lys	Gln	Lys	Glu	Lys	
			65				70						75			
Glu	Asp	Gln	Val	Leu	Ser	Tyr	Ile	Asn	Gly	Val	Thr	Thr	Ser	Lys	Pro	
				85				90						95		
Gly	Val	Ser	Leu	Val	Tyr	Ser	Met	Pro	Ser	Arg	Asn	Leu	Ser	Leu	Arg	
			100				105						110			
Leu	Glu	Gly	Leu	Gln	Glu	Lys	Asp	Ser	Gly	Pro	Tyr	Ser	Cys	Ser	Val	
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Asn	Val	Gln	Asp	Lys	Gln	Gly	Lys	Ser	Arg	Gly	His	Ser	Ile	Lys	Thr	
			130				135						140			
Leu	Glu	Leu	Asn	Val	Leu	Val	Pro	Pro	Ala	Pro	Pro	Ser	Cys	Arg	Leu	
			145				150						155			
Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr	Leu	Ser	Cys	Gln	Ser	
				165				170						175		
Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp	Asp	Arg	Gln	Leu	Pro	
			180				185						190			
Ser	Phe	Gln	Thr	Phe	Phe	Ala	Pro	Ala	Leu	Asp	Val	Ile	Arg	Gly	Ser	
			195				200						205			
Leu	Ser	Leu	Thr	Asn	Leu	Ser	Ser	Ser	Met	Ala	Gly	Val	Tyr	Val	Cys	
			210				215						220			
Lys	Ala	His	Asn	Glu	Val	Gly	Thr	Ala	Gln	Cys	Asn	Val	Thr	Leu	Glu	
			225				230						235			
Val	Ser	Thr	Gly	Pro	Gly	Ala	Ala	Val	Val	Ala	Gly	Ala	Val	Val	Gly	
				245				250						255		
Thr	Leu	Val	Gly	Leu	Gly	Leu	Leu	Ala	Gly	Leu	Val	Leu	Leu	Tyr	His	
			260				265						270			
Arg	Arg	Gly	Lys	Ala	Leu	Glu	Glu	Pro	Ala	Asn	Asp	Ile	Lys	Glu	Asp	
			275				280						285			

Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile  
 290 295 300

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg  
 305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser  
 325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly  
 340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser  
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Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser  
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Gln Ala Gly Ser Leu Val  
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 <212> DNA  
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 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<210> 41  
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<210> 42  
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 oligonucleotide probe

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<210> 47



<211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 47  
 ccgactacga ctgggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48  
 <211> 2822  
 <212> DNA  
 <213> Homo sapiens

<400> 48  
 cgccaccact gcggccaccg ccaatgaaac gctcccgcct cctagtgggtt ttttccactt 60  
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 gtgaaatacg caatggaatt gaagcctgct attgcaacat gggattttca ggaaatggtg 180  
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 ctaattgcac taacacagaa ggaagttatt attgtatgtg tgtacctggc ttcagatcca 300  
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 caaactgccca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420  
 tcagatccat aaaagaacct gtggctttgc tacaagaagt ctatagaaat tctgtgacag 480  
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540  
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 tatctgtgaa tcataggaga acacatctta caaaactcat gcacactggt gaacaagcta 720  
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 taacatttac attaagtcac cgaaaggcca cagataggta taggagtcta tgtgcatttt 1140  
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 agagaatggt ggataattac aactgcacaa aaataaaaaa tccaagctgt ggatgaccaa 2160



180						185						190				
Glu	Phe	Val	Lys	Thr	Val	Asn	Asn	Phe	Val	Gln	Arg	Asp	Thr	Phe	Val	
		195				200						205				
Val	Trp	Asp	Lys	Leu	Ser	Val	Asn	His	Arg	Arg	Thr	His	Leu	Thr	Lys	
		210				215						220				
Leu	Met	His	Thr	Val	Glu	Gln	Ala	Thr	Leu	Arg	Ile	Ser	Gln	Ser	Phe	
		225			230					235				240		
Gln	Lys	Thr	Thr	Glu	Phe	Asp	Thr	Asn	Ser	Thr	Asp	Ile	Ala	Leu	Lys	
				245					250					255		
Val	Phe	Phe	Phe	Asp	Ser	Tyr	Asn	Met	Lys	His	Ile	His	Pro	His	Met	
			260				265						270			
Asn	Met	Asp	Gly	Asp	Tyr	Ile	Asn	Ile	Phe	Pro	Lys	Arg	Lys	Ala	Ala	
		275				280						285				
Tyr	Asp	Ser	Asn	Gly	Asn	Val	Ala	Val	Ala	Phe	Leu	Tyr	Tyr	Lys	Ser	
		290				295					300					
Ile	Gly	Pro	Leu	Leu	Ser	Ser	Ser	Asp	Asn	Phe	Leu	Leu	Lys	Pro	Gln	
		305			310					315			320			
Asn	Tyr	Asp	Asn	Ser	Glu	Glu	Glu	Glu	Arg	Val	Ile	Ser	Ser	Val	Ile	
				325					330					335		
Ser	Val	Ser	Met	Ser	Ser	Asn	Pro	Pro	Thr	Leu	Tyr	Glu	Leu	Glu	Lys	
			340					345					350			
Ile	Thr	Phe	Thr	Leu	Ser	His	Arg	Lys	Val	Thr	Asp	Arg	Tyr	Arg	Ser	
		355				360						365				
Leu	Cys	Ala	Phe	Trp	Asn	Tyr	Ser	Pro	Asp	Thr	Met	Asn	Gly	Ser	Trp	
		370				375					380					
Ser	Ser	Glu	Gly	Cys	Glu	Leu	Thr	Tyr	Ser	Asn	Glu	Thr	His	Thr	Ser	
		385			390					395			400			
Cys	Arg	Cys	Asn	His	Leu	Thr	His	Phe	Ala	Ile	Leu	Met	Ser	Ser	Gly	
				405					410					415		
Pro	Ser	Ile	Gly	Ile	Lys	Asp	Tyr	Asn	Ile	Leu	Thr	Arg	Ile	Thr	Gln	
			420					425					430			
Leu	Gly	Ile	Ile	Ile	Ser	Leu	Ile	Cys	Leu	Ala	Ile	Cys	Ile	Phe	Thr	
		435				440					445					
Phe	Trp	Phe	Phe	Ser	Glu	Ile	Gln	Ser	Thr	Arg	Thr	Thr	Ile	His	Lys	
		450				455					460					





<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

<210> 55

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 55

ggatctctg agctcagg

18

<210> 56

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 56

cctagttgag tgatccttgt aag

23

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 57

atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58

<211> 2137

<212> DNA

<213> Homo sapiens

<400> 58

gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60  
cgctaagcga ggctcctcc tcccgcatg ccgaacggcc tgggcggggg caccgccgct 120

gggacaagaa gccgccgcct gcctgcccgg gcccggggag ggggctgggg ctggggccgg 180  
 aggcgggggtg tgagtgggtg tgtgcggggg gccgaggctt gatgcaatcc cgataagaaa 240  
 tgctcgggtg tcttgggcac ctaccctggg ggcgcgtaag gcgctactat ataaggctgc 300  
 cggcccgag cgcgcgcgc gtcagagcag gagecgtgcg tccaggatct agggccacga 360  
 ccatcccaac ccggcactca cagccccgca gcgcaccccg gtgcgcgcgc agcctcccgc 420  
 acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480  
 ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gcccctcgc 540  
 cttctcggac gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600  
 cctgtacacc tccggcccc acgggctctc cagctgcttc ctgcgcaccc gtgcgcagcg 660  
 cgtcgtggac tgcgcgcgg gccagagcgc gcacagtttg ctggagatca aggcagtcgc 720  
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgcga 780  
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<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu  
 1 5 10 15

Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro  
 20 25 30

His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr  
 35 40 45

Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala  
 50 55 60

Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu  
65 70 75 80

Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His  
85 90 95

Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu  
100 105 110

Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro  
115 120 125

Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser  
130 135 140

Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu  
145 150 155 160

Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro  
165 170 175

Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu  
180 185 190

Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala  
195 200 205

Val Arg Ser Pro Ser Phe Glu Lys  
210 215

<210> 60

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 60

atccgcccag atggctacaa tgtgta

26

<210> 61

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 61

gcctcccggg ctcctgagc agtgccaaac agcggcagtg ta

42



<210> 62  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 62  
 ccagtcggt gacaagccca aa 22

<210> 63  
 <211> 1295  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 cccagaagtt caagggcccc eggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60  
 cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120  
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 ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360  
 tttcaatata cggatcaaaa atgtgacaag aagtgtgagc gggaaatatc gttgtgaagt 420  
 tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tgggaagtatt 480  
 agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggg 540  
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<210> 64  
 <211> 312  
 <212> PRT  
 <213> Homo sapiens

<400> 64

Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr  
 1 5 10 15

Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro  
 20 25 30

Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu  
                   35                                  40                                  45  
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys  
                   50                                  55                                  60  
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln  
                   65                                  70                                  75                                  80  
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  
                                   85                                  90                                  95  
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser  
                                   100                                  105                                  110  
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu  
                   115                                  120                                  125  
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser  
                   130                                  135                                  140  
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly  
                   145                                  150                                  155                                  160  
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu  
                                   165                                  170                                  175  
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met  
                                   180                                  185                                  190  
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp  
                   195                                  200                                  205  
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg  
                   210                                  215                                  220  
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile  
                   225                                  230                                  235                                  240  
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu  
                                   245                                  250                                  255  
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser  
                   260                                  265                                  270  
 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn  
                   275                                  280                                  285  
 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala  
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 Gly Gly Ser Arg Gly Gln Glu Phe

305

310

&lt;210&gt; 65

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 65

atcgttgtga agttagtgcc cc

22

&lt;210&gt; 66

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 66

acctgcgata tccaacagaa ttg

23

&lt;210&gt; 67

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 67

ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc

48

&lt;210&gt; 68

&lt;211&gt; 2639

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 68

gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaag 60  
agaaagaaga ggaagatgtt gggcaacatt tatttaacat gctccacagc ccggaccctg 120  
gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180  
aaataaatga attactcaat ctccatgac catctatata tactccacct tcaaaaagta 240  
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aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggt 600
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
      20             25             30

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Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
      35             40             45

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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn  
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 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly  
 85 90 95  
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val  
 100 105 110  
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu  
 115 120 125  
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu  
 130 135 140  
 Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe  
 145 150 155 160  
 Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu  
 165 170 175  
 Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile  
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 Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe  
 195 200 205  
 Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu  
 210 215 220  
 Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser  
 225 230 235 240  
 Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu  
 245 250 255  
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 260 265 270  
 Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu  
 275 280 285  
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 Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro  
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 Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu  
 325 330 335  
 Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly

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		355					360					365			
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		370					375					380			
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							390					395			400
Glu	Phe	Gln	Gly	Gln	Asn	Val	Arg	Gln	Val	His	Phe	Arg	Asp	Met	Met
				405					410					415	
Glu	Ile	Cys	Leu	Pro	Leu	Ile	Ala	Pro	Glu	Ser	Phe	Pro	Ser	Asn	Leu
				420					425					430	
Asn	Val	Glu	Ala	Gly	Ser	Tyr	Val	Ser	Phe	His	Cys	Arg	Ala	Thr	Ala
				435					440					445	
Glu	Pro	Gln	Pro	Glu	Ile	Tyr	Trp	Ile	Thr	Pro	Ser	Gly	Gln	Lys	Leu
				450					455					460	
Leu	Pro	Asn	Thr	Leu	Thr	Asp	Lys	Phe	Tyr	Val	His	Ser	Glu	Gly	Thr
				465					470					475	480
Leu	Asp	Ile	Asn	Gly	Val	Thr	Pro	Lys	Glu	Gly	Gly	Leu	Tyr	Thr	Cys
				485					490					495	
Ile	Ala	Thr	Asn	Leu	Val	Gly	Ala	Asp	Leu	Lys	Ser	Val	Met	Ile	Lys
				500					505					510	
Val	Asp	Gly	Ser	Phe	Pro	Gln	Asp	Asn	Asn	Gly	Ser	Leu	Asn	Ile	Lys
				515					520					525	
Ile	Arg	Asp	Ile	Gln	Ala	Asn	Ser	Val	Leu	Val	Ser	Trp	Lys	Ala	Ser
				530					535					540	
Ser	Lys	Ile	Leu	Lys	Ser	Ser	Val	Lys	Trp	Thr	Ala	Phe	Val	Lys	Thr
				545					550					555	560
Glu	Asn	Ser	His	Ala	Ala	Gln	Ser	Ala	Arg	Ile	Pro	Ser	Asp	Val	Lys
				565					570					575	
Val	Tyr	Asn	Leu	Thr	His	Leu	Asn	Pro	Ser	Thr	Glu	Tyr	Lys	Ile	Cys
				580					585					590	
Ile	Asp	Ile	Pro	Thr	Ile	Tyr	Gln	Lys	Asn	Arg	Lys	Lys	Cys	Val	Asn
				595					600					605	
Val	Thr	Thr	Lys	Gly	Leu	His	Pro	Asp	Gln	Lys	Glu	Tyr	Glu	Lys	Asn
				610					615					620	

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile  
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp  
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala  
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys  
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro  
690 695 700

Thr Asn Met Ser  
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<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

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tcttctctct gaaacagtc tactgtatct ggactccaat cagatcacat ctattcccaa 420
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aattgccaac aaccctggc actgcgactg tactctacag caagtctga ggagcatggc 660
gtccaatcat gagacagccc acaacgtgat ctgtaaaacg tccgtgttgg atgaacatgc 720
tggcagacca ttctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaac 780
taccgattat gccatgctgg tcacctgtt tggctgggtc actatggtga tctcatatgt 840
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<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

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<210> 72
<211> 2290
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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 72

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&lt;210&gt; 73

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro

1

5

10

15

Ser	Pro	Leu	Leu	Ala	Cys	Trp	Gln	Pro	Ile	Leu	Leu	Leu	Val	Leu	Gly	
			20					25					30			
Ser	Val	Leu	Ser	Gly	Ser	Ala	Thr	Gly	Cys	Pro	Pro	Arg	Cys	Glu	Cys	
			35					40					45			
Ser	Ala	Gln	Asp	Arg	Ala	Val	Leu	Cys	His	Arg	Lys	Cys	Phe	Val	Ala	
			50					55					60			
Val	Pro	Glu	Gly	Ile	Pro	Thr	Glu	Thr	Arg	Leu	Leu	Asp	Leu	Gly	Lys	
			65					70					75		80	
Asn	Arg	Ile	Lys	Thr	Leu	Asn	Gln	Asp	Glu	Phe	Ala	Ser	Phe	Pro	His	
			85								90					
Leu	Glu	Glu	Leu	Glu	Leu	Asn	Glu	Asn	Ile	Val	Ser	Ala	Val	Glu	Pro	
			100								105					
Gly	Ala	Phe	Asn	Asn	Leu	Phe	Asn	Leu	Arg	Thr	Leu	Gly	Leu	Arg	Ser	
			115					120					125			
Asn	Arg	Leu	Lys	Leu	Ile	Pro	Leu	Gly	Val	Phe	Thr	Gly	Leu	Ser	Asn	
			130					135					140			
Leu	Thr	Lys	Gln	Asp	Ile	Ser	Glu	Asn	Lys	Ile	Val	Ile	Leu	Leu	Asp	
			145					150					155		160	
Tyr	Met	Phe	Gln	Asp	Leu	Tyr	Asn	Leu	Lys	Ser	Leu	Glu	Val	Gly	Asp	
			165								170					
Asn	Asp	Leu	Val	Tyr	Ile	Ser	His	Arg	Ala	Phe	Ser	Gly	Leu	Asn	Ser	
			180					185					190			
Leu	Glu	Gln	Leu	Thr	Leu	Glu	Lys	Cys	Asn	Leu	Thr	Ser	Ile	Pro	Thr	
			195					200					205			
Glu	Ala	Leu	Ser	His	Leu	His	Gly	Leu	Ile	Val	Leu	Arg	Leu	Arg	His	
			210					215					220			
Leu	Asn	Ile	Asn	Ala	Ile	Arg	Asp	Tyr	Ser	Phe	Lys	Arg	Leu	Tyr	Arg	
			225					230					235		240	
Leu	Lys	Val	Leu	Glu	Ile	Ser	His	Trp	Pro	Tyr	Leu	Asp	Thr	Met	Thr	
			245								250					
Pro	Asn	Cys	Leu	Tyr	Gly	Leu	Asn	Leu	Thr	Ser	Leu	Ser	Ile	Thr	His	
			260					265					270			
Cys	Asn	Leu	Thr	Ala	Val	Pro	Tyr	Leu	Ala	Val	Arg	His	Leu	Val	Tyr	
			275					280					285			
Leu	Arg	Phe	Leu	Asn	Leu	Ser	Tyr	Asn	Pro	Ile	Ser	Thr	Ile	Glu	Gly	
			290					295					300			

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly  
 305 310 315 320  
 Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr  
 325 330 335  
 Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu  
 340 345 350  
 Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser  
 355 360 365  
 Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg  
 370 375 380  
 Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu  
 385 390 395 400  
 Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro  
 405 410 415  
 Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln  
 420 425 430  
 Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala  
 435 440 445  
 Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His  
 450 455 460  
 Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly  
 465 470 475 480  
 Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu  
 485 490 495  
 Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu  
 500 505 510  
 His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr  
 515 520 525  
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 530 535 540  
 Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala  
 545 550 555 560  
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 565 570 575  
 Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn

580	585	590	
Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser			
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<212> DNA			
<213> Artificial Sequence			
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<400> 74			
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<210> 75			
<211> 23			
<212> DNA			
<213> Artificial Sequence			
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ataccagcta taaccaggct gcg			23
<210> 76			
<211> 52			
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<400> 77  
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<210> 78  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 78  
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<210> 79  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 79  
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<210> 80  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 oligonucleotide probe

<400> 80  
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<210> 81  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
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<400> 81  
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<210> 82

<211> 50  
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<400> 82  
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<210> 83  
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 <212> DNA  
 <213> Homo sapiens

<400> 83  
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<210> 84  
 <211> 398  
 <212> PRT  
 <213> Homo sapiens

<400> 84

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Cys	Cys	Trp	Ala	Pro	Gly	Gly	Ala	Asn	Leu	Ser	Gln	Asp	Asp	Ser	Gln
			20					25					30		
Pro	Trp	Thr	Ser	Asp	Glu	Thr	Val	Val	Ala	Gly	Gly	Thr	Val	Val	Leu
		35					40					45			
Lys	Cys	Gln	Val	Lys	Asp	His	Glu	Asp	Ser	Ser	Leu	Gln	Trp	Ser	Asn
	50					55					60				
Pro	Ala	Gln	Gln	Thr	Leu	Tyr	Phe	Gly	Glu	Lys	Arg	Ala	Leu	Arg	Asp
65					70					75					80
Asn	Arg	Ile	Gln	Leu	Val	Thr	Ser	Thr	Pro	His	Glu	Leu	Ser	Ile	Ser
				85					90					95	
Ile	Ser	Asn	Val	Ala	Leu	Ala	Asp	Glu	Gly	Glu	Tyr	Thr	Cys	Ser	Ile
			100					105					110		
Phe	Thr	Met	Pro	Val	Arg	Thr	Ala	Lys	Ser	Leu	Val	Thr	Val	Leu	Gly
		115					120					125			
Ile	Pro	Gln	Lys	Pro	Ile	Ile	Thr	Gly	Tyr	Lys	Ser	Ser	Leu	Arg	Glu
	130					135					140				
Lys	Asp	Thr	Ala	Thr	Leu	Asn	Cys	Gln	Ser	Ser	Gly	Ser	Lys	Pro	Ala
145					150					155					160
Ala	Arg	Leu	Thr	Trp	Arg	Lys	Gly	Asp	Gln	Glu	Leu	His	Gly	Glu	Pro
				165					170					175	
Thr	Arg	Ile	Gln	Glu	Asp	Pro	Asn	Gly	Lys	Thr	Phe	Thr	Val	Ser	Ser
			180					185					190		
Ser	Val	Thr	Phe	Gln	Val	Thr	Arg	Glu	Asp	Asp	Gly	Ala	Ser	Ile	Val
		195					200					205			
Cys	Ser	Val	Asn	His	Glu	Ser	Leu	Lys	Gly	Ala	Asp	Arg	Ser	Thr	Ser
	210					215					220				
Gln	Arg	Ile	Glu	Val	Leu	Tyr	Thr	Pro	Thr	Ala	Met	Ile	Arg	Pro	Asp
225					230					235					240
Pro	Pro	His	Pro	Arg	Glu	Gly	Gln	Lys	Leu	Leu	Leu	His	Cys	Glu	Gly
				245					250					255	
Arg	Gly	Asn	Pro	Val	Pro	Gln	Gln	Tyr	Leu	Trp	Glu	Lys	Glu	Gly	Ser
			260					265					270		
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		275					280					285			

<223> Description of Artificial Sequence: Synthetic



## oligonucleotide probe

<400> 87  
cctagcacag tgacgagga cttggc 26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 88  
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 89  
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<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

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gcatggcaat tccctcactc gacttttccc taatgagttc gctaactttt ataatgcggg 420  
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<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

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  1             5             10            15

```

```

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
      20             25            30

```

```

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
      35             40            45

```

```

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
      50             55            60

```

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Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
      65             70            75            80

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Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
      85             90            95

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Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His  
 100 105 110  
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly  
 115 120 125  
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp  
 130 135 140  
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile  
 145 150 155 160  
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr  
 165 170 175  
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu  
 180 185 190  
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu  
 195 200 205  
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys  
 210 215 220  
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val  
 225 230 235 240  
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr  
 245 250 255  
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro  
 260 265 270  
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr  
 275 280 285  
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala  
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 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg  
 305 310 315 320  
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala  
 325 330 335  
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly  
 340 345 350  
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala  
 355 360 365  
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp  
 370 375 380

Asn	Lys	Ile	His	Ser	Ile	Arg	Lys	Ser	His	Phe	Val	Asp	Tyr	Lys	Asn	385	390	395	400
Leu	Ile	Leu	Leu	Asp	Leu	Gly	Asn	Asn	Asn	Ile	Ala	Thr	Val	Glu	Asn	405	410		415
Asn	Thr	Phe	Lys	Asn	Leu	Leu	Asp	Leu	Arg	Trp	Leu	Tyr	Met	Asp	Ser	420	425		430
Asn	Tyr	Leu	Asp	Thr	Leu	Ser	Arg	Glu	Lys	Phe	Ala	Gly	Leu	Gln	Asn	435	440		445
Leu	Glu	Tyr	Leu	Asn	Val	Glu	Tyr	Asn	Ala	Ile	Gln	Leu	Ile	Leu	Pro	450	455		460
Gly	Thr	Phe	Asn	Ala	Met	Pro	Lys	Leu	Arg	Ile	Leu	Ile	Leu	Asn	Asn	465	470	475	480
Asn	Leu	Leu	Arg	Ser	Leu	Pro	Val	Asp	Val	Phe	Ala	Gly	Val	Ser	Leu	485	490		495
Ser	Lys	Leu	Ser	Leu	His	Asn	Asn	Tyr	Phe	Met	Tyr	Leu	Pro	Val	Ala	500	505		510
Gly	Val	Leu	Asp	Gln	Leu	Thr	Ser	Ile	Ile	Gln	Ile	Asp	Leu	His	Gly	515	520		525
Asn	Pro	Trp	Glu	Cys	Ser	Cys	Thr	Ile	Val	Pro	Phe	Lys	Gln	Trp	Ala	530	535		540
Glu	Arg	Leu	Gly	Ser	Glu	Val	Leu	Met	Ser	Asp	Leu	Lys	Cys	Glu	Thr	545	550	555	560
Pro	Val	Asn	Phe	Phe	Arg	Lys	Asp	Phe	Met	Leu	Leu	Ser	Asn	Asp	Glu	565	570		575
Ile	Cys	Pro	Gln	Leu	Tyr	Ala	Arg	Ile	Ser	Pro	Thr	Leu	Thr	Ser	His	580	585		590
Ser	Lys	Asn	Ser	Thr	Gly	Leu	Ala	Glu	Thr	Gly	Thr	His	Ser	Asn	Ser	595	600		605
Tyr	Leu	Asp	Thr	Ser	Arg	Val	Ser	Ile	Ser	Val	Leu	Val	Pro	Gly	Leu	610	615		620
Leu	Leu	Val	Phe	Val	Thr	Ser	Ala	Phe	Thr	Val	Val	Gly	Met	Leu	Val	625	630	635	640
Phe	Ile	Leu	Arg	Asn	Arg	Lys	Arg	Ser	Lys	Arg	Arg	Asp	Ala	Asn	Ser	645	650		655
Ser	Ala	Ser	Glu	Ile	Asn	Ser	Leu	Gln	Thr	Val	Cys	Asp	Ser	Ser	Tyr				

660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp  
675 680 685

Cys Gly Ser His Ser Leu Ser Asp  
690 695

<210> 92  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 92  
gttggatctg ggcaacaata ac 22

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 93  
attgttgatgc aggctgagtt taag 24

<210> 94  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 94  
ggtggctata catggatagc aattacctgg acacgctgtc ccggg 45

<210> 95  
<211> 2226  
<212> DNA  
<213> Homo sapiens

<400> 95  
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gctgcaccgg gcttggcagc gctccgcaca catttcctgt cgcggcctaa gggaaactgt 120  
tgcccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgctcggg agcgagggcg 180

gaggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240  
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 gttgat 2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

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 20 25 30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln  
 35 40 45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val  
 50 55 60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly  
 65 70 75 80  
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu  
 85 90 95  
 Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly  
 100 105 110  
 Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu  
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 Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala  
 130 135 140  
 Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met  
 145 150 155 160  
 Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu  
 165 170 175  
 Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr  
 180 185 190  
 Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro  
 195 200 205  
 Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val  
 210 215 220  
 Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly  
 225 230 235 240  
 Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys  
 245 250 255  
 Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu  
 260 265 270  
 Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr  
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 Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg  
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 Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro  
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<210> 97
<211> 24
<212> DNA
<213> Artificial Sequence
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<400> 97  
tggaaggaga tqcgaatgcca cctg 24

<220>  
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<400> 98
tgaccagtgg ggaaggacag                20
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<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 99  
 acagagcaga gggcgcttg 20  
  
 <210> 100  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 100  
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 <210> 101  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 101  
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 <210> 102  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe  
  
 <400> 102  
 acagctcccg atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct 50  
  
 <210> 103  
 <211> 2026  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 103

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tctaaatcaa tgcttaataa aatattttta aaggaaaaaa aaaaaa 2026

```

&lt;210&gt; 104

&lt;211&gt; 415

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 104

```

Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
  1                      5                      10                      15

Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
                20                      25                      30

Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
                35                      40                      45

Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
  50                      55                      60

```

Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu  
 65 70 75 80  
 Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly  
 85 90 95  
 His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro  
 100 105 110  
 Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser  
 115 120 125  
 Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala  
 130 135 140  
 Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg  
 145 150 155 160  
 Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro  
 165 170 175  
 Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu  
 180 185 190  
 Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys  
 195 200 205  
 Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala  
 210 215 220  
 Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val  
 225 230 235 240  
 Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu  
 245 250 255  
 Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu  
 260 265 270  
 Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr  
 275 280 285  
 Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr  
 290 295 300  
 Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly  
 305 310 315 320  
 Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val  
 325 330 335  
 Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala

090439  
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 0704  
 0704

340	345	350
Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro		
355	360	365
Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu		
370	375	380
Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys		
385	390	395
Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys		
405	410	415

&lt;210&gt; 105

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 105

ccgattcata gacctcgaga gt

22

&lt;210&gt; 106

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 106

gtcaaggagt cctccacaat ac

22

&lt;210&gt; 107

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 107

gtgtacaatg gccatgcaa tggccagcgc attggccgct tctgt

45

&lt;210&gt; 108

&lt;211&gt; 1838

&lt;212&gt; DNA

<213> Homo sapiens

<400> 108

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tgttcaccac atccccacac cccattgcca cttatttatt catctcagga aataaagaaa 1800
ggtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

```

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

```

Met Ala Pro Trp Pro Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
  1             5             10             15

```

```

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
      20             25             30

```

```

Pro Pro Pro Gln Ser Ser Pro Pro Pro Gln Pro His Pro Cys His Thr
      35             40             45

```

```

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
      50             55             60

```



Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln  
           355                                  360                                  365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys  
      370                                  375                                  380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met  
 385                                  390                                  395                                  400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe  
                                   405                                  410                                  415

Ile Lys Gly Arg  
                   420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 110

cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 111

attctgcgtg aacactgagg gc 22

<210> 112

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
           oligonucleotide probe

<400> 112

atctgcttgt agccctcggc ac 22

<210> 113

<211> 1616  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> modified\_base  
 <222> (1461)  
 <223> a, t, c or g

<400> 113  
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 cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180  
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 aaagtccctc accaccactc tggacctaa acctgggggt aagtgtgggt tgtgcatccc 1560  
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<210> 114  
 <211> 366  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 1 5 10 15  
 Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu  
 20 25 30  
 Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met  
 35 40 45





Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser  
                   340                                  345                                  350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro  
                   355                                  360                                  365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 115

aggactgccca taacttgctt g 21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc 22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
                   oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc 45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

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 aaggcgcaag tcgagaggaa actgttgtgc ctcttcata tggcgatcct gttgtgtccc 120  
 ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180

```

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```

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

```

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
  1              5              10             15

```

```

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
      20              25              30

```

```

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
      35              40              45

```

```

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
      50              55              60

```

```

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
      65              70              75              80

```

```

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
      85              90              95

```



<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 121  
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 <210> 122  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 122  
 acacctggtt caaagatggg 20  
  
 <210> 123  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 123  
 taggaagagt tgctgaaggc acgg 24  
  
 <210> 124  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic  
         oligonucleotide probe  
  
 <400> 124  
 ttgccttact caggtgctac 20  
  
 <210> 125  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

&lt;400&gt; 125

actcagcagt ggtaggaaag

20

&lt;210&gt; 126

&lt;211&gt; 1210

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 126

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gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctgggactag 120  
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tcttcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080  
agctaggatg gggaaacctgc cacagccaga actgaggggc tggccccagg cagctcccag 1140  
ggggtagaac ggccctgtgc ttaagacact ccctgctgcc ccgtctgagg gtggcgatta 1200  
aagttgcttc 1210

&lt;210&gt; 127

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala  
1 5 10 15  
Leu Gly Leu Ala Leu Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu  
20 25 30  
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly  
35 40 45  
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser  
50 55 60  
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys  
65 70 75 80

```

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
      85                      90                      95

Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
      100                      105                      110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
      115                      120                      125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
      130                      135                      140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
      145                      150                      155                      160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
      165                      170                      175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
      180                      185                      190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
      195                      200                      205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
      210                      215                      220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala
      225                      230                      235                      240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
      245                      250                      255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
      260                      265                      270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
      275                      280

```

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

<210> 129

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 130

gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc

50

<210> 131

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (1837)

<223> a, t, c or g

<400> 131

```

cccacgcgtc cgggtctcgtc cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
gggttagact ggcgggggga ggaggcggag gagggaagga agctgcatgc atgagacca 120
cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcgccctt gcacagctca 300
cgggcggggt cgatgacctt caagtgtgtg ctgaccccg cttcccgag aatggcttca 360
ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaactg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaate atcacttgct 600
atgaaggatt caagatccgg taccgccacc tacacaatat ggtttcatta tgcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
atcgctgctt tcccggattt aaacttgatg ggtctgcgta tcttgagtgc ttacaaaacc 840
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ctccaatggt gagtacgga gatttcgtct gccaccgcg gccttgtgag cgctacaacc 960
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acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaactag 1080
agcaaacgtg gccacgacc catgagaccc tctgaccac gtggaagatt gtggcggttca 1140

```



```

cggcaaccag tgtgctgctg gtgctgctgc tcgtcatcct ggccaggatg ttccagacca 1200
agttcaaggc ccactttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
ttgtggtggt agacggcgtg cccgtcatgc tcccgtccta tgacgaagct gtgagtggcg 1320
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ctcccagggtg ccaagagagc acccaccctg cttcggacaa ccctgacata attgccagca 1560
cggcagagga ggtggcatcc accagcccag gcacccatca tgcccactgg gtgttgttcc 1620
taagaaactg attgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtagaggc tggaagcttg atcaagtcct 1800
gtttcttctt gacacagact gattaaaaat taaaagnaaa aaa 1843

```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

```

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
  1             5             10             15

```

```

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
      20             25             30

```

```

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
      35             40             45

```

```

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
      50             55             60

```

```

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
      65             70             75             80

```

```

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
      85             90             95

```

```

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
     100             105             110

```

```

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
     115             120             125

```

```

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
     130             135             140

```

```

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
     145             150             155             160

```

```

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
     165             170             175

```

```

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn

```

180					185					190					
Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr
		195					200					205			
Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys
	210					215					220				
Leu	Gln	Asn	Leu	Ile	Trp	Ser	Ser	Ser	Pro	Pro	Arg	Cys	Leu	Ala	Leu
225					230					235					240
Glu	Ala	Gln	Val	Cys	Pro	Leu	Pro	Pro	Met	Val	Ser	His	Gly	Asp	Phe
				245					250					255	
Val	Cys	His	Pro	Arg	Pro	Cys	Glu	Arg	Tyr	Asn	His	Gly	Thr	Val	Val
			260					265					270		
Glu	Phe	Tyr	Cys	Asp	Pro	Gly	Tyr	Ser	Leu	Thr	Ser	Asp	Tyr	Lys	Tyr
		275					280					285			
Ile	Thr	Cys	Gln	Tyr	Gly	Glu	Trp	Phe	Pro	Ser	Tyr	Gln	Val	Tyr	Cys
	290					295					300				
Ile	Lys	Ser	Glu	Gln	Thr	Trp	Pro	Ser	Thr	His	Glu	Thr	Leu	Leu	Thr
305					310					315					320
Thr	Trp	Lys	Ile	Val	Ala	Phe	Thr	Ala	Thr	Ser	Val	Leu	Leu	Val	Leu
				325					330					335	
Leu	Leu	Val	Ile	Leu	Ala	Arg	Met	Phe	Gln	Thr	Lys	Phe	Lys	Ala	His
			340					345					350		
Phe	Pro	Pro	Arg	Gly	Pro	Pro	Arg	Ser	Ser	Ser	Ser	Asp	Pro	Asp	Phe
		355					360					365			
Val	Val	Val	Asp	Gly	Val	Pro	Val	Met	Leu	Pro	Ser	Tyr	Asp	Glu	Ala
	370					375					380				
Val	Ser	Gly	Gly	Leu	Ser	Ala	Leu	Gly	Pro	Gly	Tyr	Met	Ala	Ser	Val
385					390					395					400
Gly	Gln	Gly	Cys	Pro	Leu	Pro	Val	Asp	Asp	Gln	Ser	Pro	Pro	Ala	Tyr
				405					410					415	
Pro	Gly	Ser	Gly	Asp	Thr	Asp	Thr	Gly	Pro	Gly	Glu	Ser	Glu	Thr	Cys
			420					425					430		
Asp	Ser	Val	Ser	Gly	Ser	Ser	Glu	Leu	Leu	Gln	Ser	Leu	Tyr	Ser	Pro
		435					440					445			
Pro	Arg	Cys	Gln	Glu	Ser	Thr	His	Pro	Ala	Ser	Asp	Asn	Pro	Asp	Ile
	450					455					460				

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His  
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn  
 485 490

<210> 133  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 133  
 atctcctatc gctgctttcc cgg 23

<210> 134  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 134  
 agccaggatc gcagtaaaac tcc 23

<210> 135  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 135  
 atttaaactt gatgggtctg cgtatcttga gtgcttaca aaccttatct 50

<210> 136  
 <211> 1815  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 cccacgcgtc cgtccgcgc cctccccccc gcctcccgctg cggtcgcgtg gtggcctaga 60  
 gatgctgctg ccgcgggttg agttgtcgcg cagcctctg cccgccagcc cgtccaccg 120  
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180  
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240  
 tgagtgcctc ggatttgac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300

ggcccttggtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360  
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420  
 agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480  
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540  
 ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcgga 600  
 gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggagggccct 660  
 acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720  
 ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780  
 cacctgtact tccagaagaa acacaggaag aagatgccaa aaaaacattt aaagaaagta 840  
 gagaagctgc cttgaatctg gcctacatcc taatccccag cattccccct ctcctcctcc 900  
 ttgtggtcac cacagttgta tgttgggttt ggatctgtag aaaaagaaaa cgggagcagc 960  
 cagaccctag cacaagaag caacacacca tctggccctc tcctcaccag ggaaacagcc 1020  
 cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080  
 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140  
 tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200  
 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaatgg 1260  
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320  
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380  
 ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440  
 tccccacgac ctctgttgg acccccacgt tttggctgta tcctttatcc cagccagtca 1500  
 tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560  
 aaatgtcact tggttgggtg tatctaact ttaagggaca gagctttacc tggcagtgat 1620  
 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680  
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740  
 ttggcctgtg catcggaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800  
 agcaggaaaa aaaaa 1815

<210> 137

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu  
 1 5 10 15

Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu  
 20 25 30

Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro  
 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe  
 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser  
 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn  
 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu  
 100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr  
 115 120 125  
 Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser  
 130 135 140  
 Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro  
 145 150 155 160  
 Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys  
 165 170 175  
 Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala  
 180 185 190  
 Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro  
 195 200 205  
 Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys  
 210 215 220  
 Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser  
 225 230 235 240  
 Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val  
 245 250 255  
 Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys  
 260 265 270  
 Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp  
 275 280 285  
 Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala  
 290 295 300  
 Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly  
 305 310 315 320  
 Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val  
 325 330 335  
 Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly  
 340 345 350  
 Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg  
 355 360 365  
 Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr  
 370 375 380

&lt;210&gt; 138

<211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 138  
 gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 139  
 aagccaaaga agcctgcagg aggg 24

<210> 140  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 140  
 cagtccaagc ataaaggtcc tggc 24

<210> 141  
 <211> 1514  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
 ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60  
 gcatccgcag gttcccgcgg acttgggggc gcccgctgag ccccggcgcc cgcagaagac 120  
 ttgtgtttgc ctctgcagc ctcaaccggg agggcagcga gggcctacca ccatgatcac 180  
 tgggtgtgttc agcatgcgct tgtggacccc agtgggcgtc ctgacctcgc tggcgctactg 240  
 cctgcaccag cggcggggtgg ccctggccga gctgcaggag gccgatggcc agtgtccggt 300  
 cgaccgcagc ctgctgaagt tgaaaatggt gcaggctcgtg ttctgacacg gggctcggag 360  
 tcctctcaag ccgctcccgc tggaggagca ggtagagtgg aacccccagc tattagaggt 420  
 cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480  
 ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540  
 gctgaccaag gtgggcatgc agcaaagtgt tgccttggga gagagactga ggaagaacta 600  
 tgtggaagac attccctttc tttcaccaac cttcaacca caggaggtct ttattcggtc 660  
 cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720



Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His  
                   180                                  185                                  190  
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys  
                   195                                  200                                  205  
 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu  
                   210                                  215                                  220  
 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly  
                   225                                  230                                  235                                  240  
 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val  
                                   245                                  250                                  255  
 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg  
                                   260                                  265                                  270  
 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile  
                                   275                                  280                                  285  
 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe  
                   290                                  295                                  300  
 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr  
                   305                                  310                                  315                                  320  
 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val  
                                   325                                  330                                  335  
 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp  
                                   340                                  345                                  350  
 Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu  
                   355                                  360                                  365  
 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val  
                   370                                  375                                  380  
 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn  
                   385                                  390                                  395                                  400  
 Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys  
                                   405                                  410                                  415  
 Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu  
                                   420                                  425

&lt;210&gt; 143

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 144

gcagctctat taccacggga agga

24

<210> 145

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 145

tccttcccggt ggtaatagag ctgc

24

<210> 146

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 146

ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147

<211> 1686

<212> DNA

<213> Homo sapiens

<400> 147

ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60  
cttaaatttc agctcatcac cttcacctgc cttgggtcatg gctctgctat tctccttgat 120  
ccttgccatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctggtggg 180

```

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccgt 240
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ggctcctcat caatcagtca gttgcacagg aacagaagat acattggctc agtgtgagca 420
agaagaagtt tatgattggt cacatgatga agatgctggg gcatcgtgtg agaaccacaga 480
gagctctttc tccccagtc cagagggtgt caggctggct gacggccctg ggcattgcaa 540
gggacgcgtg gaagtgaagc accagaacca gtggtatacc gtgtgccaga caggctggag 600
cctccggggc gcaaagggtg tgtgccggca gctgggatgt gggagggtg tactgactca 660
aaaacgctgc aacaagcatg cctatggccg aaaacccatc tggctgagcc agatgtcatg 720
ctcaggacga gaagcaaccc ttcaggattg cccttctggg ccttggggga agaacacctg 780
caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
aggagacaac ctctgctctg ggcgactgga ggtgctgcac aagggcgat ggggctctgt 900
ctgtgatgac aactggggag aaaaggagga ccagggtgga tgcaagcaac tgggctgtgg 960
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ctggctggat aatgttcgtt gctcagggga ggagcagtc ctggagcagt gccagcacag 1080
atthtggggg tttcacgact gcacccacca ggaagatgtg gctgtcatct gctcagtgt 1140
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ttcaaa 1686

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<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly  
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg  
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val  
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu  
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu  
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys  
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr  
100 105 110

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Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
    115                      120                      125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
    130                      135                      140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
    145                      150                      155                      160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
                      165                      170                      175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
                      180                      185                      190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
    195                      200                      205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
    210                      215                      220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
    225                      230                      235                      240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
                      245                      250                      255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
    260                      265                      270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
    275                      280                      285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
    290                      295                      300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
    305                      310                      315                      320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
                      325                      330                      335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
    340                      345

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<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

## oligonucleotide probe

<400> 149  
ttcagctcat caccttcacc tgcc 24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 150  
ggctcataca aaataccact aggg 24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 151  
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt 50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152  
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gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180  
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gaatgctgtg gtggtgatca caggcgccac ctccaggctg ggcaaagaat gtgcaaaagt 300  
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gctcatcaga gaacttaccg cttctcatgc caccaagggtg cagacacaca agccttactt 420  
ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480  
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cttactgcct tccttggtcg tttatcttcg aactctggct cctgggctct tcttcagcct 1020  
catggcctcc agggccagaa aagagcggaa atccaagaac tcctagtact ctgaccagcc 1080

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agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
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gtgcagatct gctggcagag gacaatcaaa aacgacaaca agcttcttcc caggggtgagg 1260
ggaaacactt aaggaataaa tatggagctg gggtttaaca ctaaaaacta gaaataaaca 1320
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cttggccgcc atggcccaac ttgtttattg cagcttataa tggttac 1427

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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
  1                      5                      10                      15

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Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20                      25                      30

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Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
          35                      40                      45

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Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
          50                      55                      60

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Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
          65                      70                      75                      80

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Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85                      90                      95

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Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala
          100                     105                     110

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Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
          115                     120                     125

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Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
          130                     135                     140

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Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
          145                     150                     155                     160

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Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165                     170                     175

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Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
          180                     185                     190

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Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
          195                     200                     205

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Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr

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210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg  
 225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu  
 245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val  
 260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu  
 275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu  
 290 295 300

Arg Lys Ser Lys Asn Ser  
 305 310

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 154  
 ggtgctaaac tgggtgctctg tggc 24

<210> 155  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 155  
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<210> 156  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 156  
tcatactgtt ccatctcggc acgc 24

<210> 157  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 157  
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158  
<211> 1771  
<212> DNA  
<213> Homo sapiens

<400> 158  
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<210> 159

<400>	159														
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Cys	Ser	Leu	Glu	Ser	Phe	Val	Lys	Leu	Phe	Ile	Pro	Lys	Arg	Arg	Lys
			20					25					30		
Ser	Val	Thr	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	His	Gly	Ile
		35					40					45			
Gly	Arg	Leu	Thr	Ala	Tyr	Glu	Phe	Ala	Lys	Leu	Lys	Ser	Lys	Leu	Val
	50					55					60				
Leu	Trp	Asp	Ile	Asn	Lys	His	Gly	Leu	Glu	Glu	Thr	Ala	Ala	Lys	Cys
65					70					75					80
Lys	Gly	Leu	Gly	Ala	Lys	Val	His	Thr	Phe	Val	Val	Asp	Cys	Ser	Asn
				85					90					95	
Arg	Glu	Asp	Ile	Tyr	Ser	Ser	Ala	Lys	Lys	Val	Lys	Ala	Glu	Ile	Gly
			100					105					110		
Asp	Val	Ser	Ile	Leu	Val	Asn	Asn	Ala	Gly	Val	Val	Tyr	Thr	Ser	Asp
		115					120					125			
Leu	Phe	Ala	Thr	Gln	Asp	Pro	Gln	Ile	Glu	Lys	Thr	Phe	Glu	Val	Asn
	130					135					140				
Val	Leu	Ala	His	Phe	Trp	Thr	Thr	Lys	Ala	Phe	Leu	Pro	Ala	Met	Thr
145					150					155					160
Lys	Asn	Asn	His	Gly	His	Ile	Val	Thr	Val	Ala	Ser	Ala	Ala	Gly	His
				165					170					175	
Val	Ser	Val	Pro	Phe	Leu	Leu	Ala	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala
			180					185					190		
Val	Gly	Phe	His	Lys	Thr	Leu	Thr	Asp	Glu	Leu	Ala	Ala	Leu	Gln	Ile
		195					200					205			
Thr	Gly	Val	Lys	Thr	Thr	Cys	Leu	Cys	Pro	Asn	Phe	Val	Asn	Thr	Gly
	210					215					220				
Phe	Ile	Lys	Asn	Pro	Ser	Thr	Ser	Leu	Gly	Pro	Thr	Leu	Glu	Pro	Glu
225					230					235					240
Glu	Val	Val	Asn	Arg	Leu	Met	His	Gly	Ile	Leu	Thr	Glu	Gln	Lys	Met
				245					250					255	





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<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met  
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Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser  
 20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr  
 35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly  
 50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val

65		70		75		80
Asn Lys Thr Tyr	Asn Ser Asn Leu Phe	Phe Trp Phe Phe Pro Ala Gln				
	85	90	95			
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro		100	105	110		
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val		115	120	125		
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr		130	135	140		
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser		145	150	155	160	
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala		165	170	175		
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu		180	185	190		
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys		195	200	205		
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg		210	215	220		
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser		225	230	235	240	
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile		245	250	255		
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His		260	265	270		
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu		275	280	285		
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr		290	295	300		
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys		305	310	315	320	
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro		325	330	335		
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly		340	345	350		

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Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys  
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Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn  
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Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu  
 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys  
 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile  
 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His  
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Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg  
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Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly  
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<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 165

ttccatgcc cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<400> 166

tgcatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 167

agctctcaga ggctgggtcat aggg

24

&lt;210&gt; 168

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 168

gtcgggccctt tcccaggact gaacatgaag agttatgccg gcttctctcac

50

&lt;210&gt; 169

&lt;211&gt; 2477

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

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cgagggtctt tccgggtccg gaatggcaca tgtgggaatc ccagtcttgt tggctacaac 60
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 Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly  
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 225 230 235 240  
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 275 280 285  
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 His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala  
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 420 425 430  
 Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr  
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 Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn

450                      455                      460  
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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20

<210> 172

<211> 24

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<213> Artificial Sequence

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<400> 172

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24

<210> 173

<211> 43

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe



<400> 173  
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<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

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<223> Any amino acid

<400> 175

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Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
          20             25             30

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Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
          35             40             45

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Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
          50             55             60

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Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
          65             70             75             80

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Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
          85             90             95

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Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
          100            105            110

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Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
          115            120            125

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Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
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Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu  
 145 150 155 160  
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp  
 165 170 175  
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro  
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 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp  
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 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile  
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 260 265 270  
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly  
 275 280 285  
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala  
 290 295 300  
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly  
 305 310 315 320  
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys  
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 Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly  
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 Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile  
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 370 375 380  
 Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu  
 385 390 395 400  
 Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu  
 405 410 415  
 Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu  
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Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His  
435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp  
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Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val  
465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn  
485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp  
500 505 510

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser  
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr  
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr  
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val  
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln  
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln  
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Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr  
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Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys  
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<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

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aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttga 180  
ggaatccgac acgtgacggg ctgtccgccc tctcagacta gaggagcgct gtaaaccgcca 240  
tggtcccaa gaagctgtcc tgccttcgtt ccctgctgct gccgctcagc ctgacgctac 300  
tgctgcccc ggcagacact cggtcgttcg tagtggatag gggtcacgac cggtttctcc 360  
tagacggggc ccggttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420

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gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660
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<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu  
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val  
20 25 30

Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr  
35 40 45

Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala  
50 55 60

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Arg | Leu | Leu | Lys | Met | Arg | Trp | Ser | Gly | Leu | Asn | Ala | Ile | Gln | Phe | 65  | 70  | 75  | 80  |
| Tyr | Val | Pro | Trp | Asn | Tyr | His | Glu | Pro | Gln | Pro | Gly | Val | Tyr | Asn | Phe | 85  | 90  | 95  |     |
| Asn | Gly | Ser | Arg | Asp | Leu | Ile | Ala | Phe | Leu | Asn | Glu | Ala | Ala | Leu | Ala | 100 | 105 | 110 |     |
| Asn | Leu | Leu | Val | Ile | Leu | Arg | Pro | Gly | Pro | Tyr | Ile | Cys | Ala | Glu | Trp | 115 | 120 | 125 |     |
| Glu | Met | Gly | Gly | Leu | Pro | Ser | Trp | Leu | Leu | Arg | Lys | Pro | Glu | Ile | His | 130 | 135 | 140 |     |
| Leu | Arg | Thr | Ser | Asp | Pro | Asp | Phe | Leu | Ala | Ala | Val | Asp | Ser | Trp | Phe | 145 | 150 | 155 | 160 |
| Lys | Val | Leu | Leu | Pro | Lys | Ile | Tyr | Pro | Trp | Leu | Tyr | His | Asn | Gly | Gly | 165 | 170 | 175 |     |
| Asn | Ile | Ile | Ser | Ile | Gln | Val | Glu | Asn | Glu | Tyr | Gly | Ser | Tyr | Arg | Ala | 180 | 185 | 190 |     |
| Cys | Asp | Phe | Ser | Tyr | Met | Arg | His | Leu | Ala | Gly | Leu | Phe | Arg | Ala | Leu | 195 | 200 | 205 |     |
| Leu | Gly | Glu | Lys | Ile | Leu | Leu | Phe | Thr | Thr | Asp | Gly | Pro | Glu | Gly | Leu | 210 | 215 | 220 |     |
| Lys | Cys | Gly | Ser | Leu | Arg | Gly | Leu | Tyr | Thr | Thr | Val | Asp | Phe | Gly | Pro | 225 | 230 | 235 | 240 |
| Ala | Asp | Asn | Met | Thr | Lys | Ile | Phe | Thr | Leu | Leu | Arg | Lys | Tyr | Glu | Pro | 245 | 250 | 255 |     |
| His | Gly | Pro | Leu | Val | Asn | Ser | Glu | Tyr | Tyr | Thr | Gly | Trp | Leu | Asp | Tyr | 260 | 265 | 270 |     |
| Trp | Gly | Gln | Asn | His | Ser | Thr | Arg | Ser | Val | Ser | Ala | Val | Thr | Lys | Gly | 275 | 280 | 285 |     |
| Leu | Glu | Asn | Met | Leu | Lys | Leu | Gly | Ala | Ser | Val | Asn | Met | Tyr | Met | Phe | 290 | 295 | 300 |     |
| His | Gly | Gly | Thr | Asn | Phe | Gly | Tyr | Trp | Asn | Gly | Ala | Asp | Lys | Lys | Gly | 305 | 310 | 315 | 320 |
| Arg | Phe | Leu | Pro | Ile | Thr | Thr | Ser | Tyr | Asp | Tyr | Asp | Ala | Pro | Ile | Ser | 325 | 330 | 335 |     |
| Glu | Ala | Gly | Asp | Pro | Thr | Pro | Lys | Leu | Phe | Ala | Leu | Arg | Asp | Val | Ile |     |     |     |     |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 340 |     | 345 |     | 350 |     |     |     |     |     |     |     |     |     |     |
| Ser | Lys | Phe | Gln | Glu | Val | Pro | Leu | Gly | Pro | Leu | Pro | Pro | Pro | Ser | Pro |
|     | 355 |     |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Met | Met | Leu | Gly | Pro | Val | Thr | Leu | His | Leu | Val | Gly | His | Leu | Leu |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Ala | Phe | Leu | Asp | Leu | Leu | Cys | Pro | Arg | Gly | Pro | Ile | His | Ser | Ile | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Pro | Met | Thr | Phe | Glu | Ala | Val | Lys | Gln | Asp | His | Gly | Phe | Met | Leu | Tyr |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Arg | Thr | Tyr | Met | Thr | His | Thr | Ile | Phe | Glu | Pro | Thr | Pro | Phe | Trp | Val |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Pro | Asn | Asn | Gly | Val | His | Asp | Arg | Ala | Tyr | Val | Met | Val | Asp | Gly | Val |
|     | 435 |     |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |
| Phe | Gln | Gly | Val | Val | Glu | Arg | Asn | Met | Arg | Asp | Lys | Leu | Phe | Leu | Thr |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |
| Gly | Lys | Leu | Gly | Ser | Lys | Leu | Asp | Ile | Leu | Val | Glu | Asn | Met | Gly | Arg |
| 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Leu | Ser | Phe | Gly | Ser | Asn | Ser | Ser | Asp | Phe | Lys | Gly | Leu | Leu | Lys | Pro |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |     |
| Pro | Ile | Leu | Gly | Gln | Thr | Ile | Leu | Thr | Gln | Trp | Met | Met | Phe | Pro | Leu |
|     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |     |     |
| Lys | Ile | Asp | Asn | Leu | Val | Lys | Trp | Trp | Phe | Pro | Leu | Gln | Leu | Pro | Lys |
|     | 515 |     |     |     |     |     | 520 |     |     |     |     | 525 |     |     |     |
| Trp | Pro | Tyr | Pro | Gln | Ala | Pro | Ser | Gly | Pro | Thr | Phe | Tyr | Ser | Lys | Thr |
|     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |     |     |     |     |
| Phe | Pro | Ile | Leu | Gly | Ser | Val | Gly | Asp | Thr | Phe | Leu | Tyr | Leu | Pro | Gly |
| 545 |     |     |     |     | 550 |     |     |     |     | 555 |     |     |     |     | 560 |
| Trp | Thr | Lys | Gly | Gln | Val | Trp | Ile | Asn | Gly | Phe | Asn | Leu | Gly | Arg | Tyr |
|     |     |     |     | 565 |     |     |     |     | 570 |     |     |     |     | 575 |     |
| Trp | Thr | Lys | Gln | Gly | Pro | Gln | Gln | Thr | Leu | Tyr | Val | Pro | Arg | Phe | Leu |
|     |     |     | 580 |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Leu | Phe | Pro | Arg | Gly | Ala | Leu | Asn | Lys | Ile | Thr | Leu | Leu | Glu | Leu | Glu |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |
| Asp | Val | Pro | Leu | Gln | Pro | Gln | Val | Gln | Phe | Leu | Asp | Lys | Pro | Ile | Leu |
|     | 610 |     |     |     |     | 615 |     |     |     |     | 620 |     |     |     |     |





<210> 182  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 182  
 tggcaccag aatggtgttg gctc

24

<210> 183  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 183  
 cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184  
 <211> 1947  
 <212> DNA  
 <213> Homo sapiens

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 gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata cctttgaagg 180  
 aatattcttt cgaaaaagtc agagaagaga gcagtttttag tgacattcca gatgtcaaaa 240  
 acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300  
 ttggtgtgtt cttgtcagaa gttagtgaat ataaacttag ggaaattagt ttgaaccatg 360  
 agtggacatt tgaaaaactc aggcagcaca tttcacgcaa cgcccaggac aagcaggagt 420  
 tgcattctgt catgctgtcg ggggtgcccg atgctgtctt tgacctcaca gacctggatg 480  
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 ttttcagcct ctctaattta caggaaactg atttaaagtc caataacatt cgcacaattg 1020  
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 tgcagcattt gcatatcact gggaacaaag tggacattct gccaaaacaa ttgttttaaa 1320



Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu  
 195 200 205  
 Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu  
 210 215 220  
 Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser  
 225 230 235 240  
 Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu  
 245 250 255  
 Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn  
 260 265 270  
 Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys  
 275 280 285  
 Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln  
 290 295 300  
 Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile  
 305 310 315 320  
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn  
 325 330 335  
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu  
 340 345 350  
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val  
 355 360 365  
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile  
 370 375 380  
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu  
 385 390 395 400  
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys  
 405 410 415  
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser  
 420 425 430  
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu  
 435 440 445  
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg  
 450 455 460  
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr

465                      470                      475                      480  
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 Phe Ala Asn Gly Ile  
                          500

<210> 186  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 186  
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<210> 187  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
                          oligonucleotide probe

<400> 187  
 gaccaacttt ctctgggagt gagg                      24

<210> 188  
 <211> 47  
 <212> DNA  
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<220>  
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                          oligonucleotide probe

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<210> 189  
 <211> 2917  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
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&lt;210&gt; 190

&lt;211&gt; 607

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Val | Arg | Arg | Leu | Met | Pro | Leu | Thr | Leu | Leu | Ile | Leu | Ser | 1   | 5   | 10  | 15  |
| Cys | Leu | Ala | Glu | Leu | Thr | Met | Ala | Glu | Ala | Glu | Gly | Asn | Ala | Ser | Cys | 20  | 25  | 30  |     |
| Thr | Val | Ser | Leu | Gly | Gly | Ala | Asn | Met | Ala | Glu | Thr | His | Lys | Ala | Met | 35  | 40  | 45  |     |
| Ile | Leu | Gln | Leu | Asn | Pro | Ser | Glu | Asn | Cys | Thr | Trp | Thr | Ile | Glu | Arg | 50  | 55  | 60  |     |
| Pro | Glu | Asn | Lys | Ser | Ile | Arg | Ile | Ile | Phe | Ser | Tyr | Val | Gln | Leu | Asp | 65  | 70  | 75  | 80  |
| Pro | Asp | Gly | Ser | Cys | Glu | Ser | Glu | Asn | Ile | Lys | Val | Phe | Asp | Gly | Thr | 85  | 90  | 95  |     |
| Ser | Ser | Asn | Gly | Pro | Leu | Leu | Gly | Gln | Val | Cys | Ser | Lys | Asn | Asp | Tyr | 100 | 105 | 110 |     |
| Val | Pro | Val | Phe | Glu | Ser | Ser | Ser | Ser | Thr | Leu | Thr | Phe | Gln | Ile | Val | 115 | 120 | 125 |     |
| Thr | Asp | Ser | Ala | Arg | Ile | Gln | Arg | Thr | Val | Phe | Val | Phe | Tyr | Tyr | Phe | 130 | 135 | 140 |     |
| Phe | Ser | Pro | Asn | Ile | Ser | Ile | Pro | Asn | Cys | Gly | Gly | Tyr | Leu | Asp | Thr | 145 | 150 | 155 | 160 |
| Leu | Glu | Gly | Ser | Phe | Thr | Ser | Pro | Asn | Tyr | Pro | Lys | Pro | His | Pro | Glu | 165 | 170 | 175 |     |
| Leu | Ala | Tyr | Cys | Val | Trp | His | Ile | Gln | Val | Glu | Lys | Asp | Tyr | Lys | Ile | 180 | 185 | 190 |     |
| Lys | Leu | Asn | Phe | Lys | Glu | Ile | Phe | Leu | Glu | Ile | Asp | Lys | Gln | Cys | Lys | 195 | 200 | 205 |     |
| Phe | Asp | Phe | Leu | Ala | Ile | Tyr | Asp | Gly | Pro | Ser | Thr | Asn | Ser | Gly | Leu | 210 | 215 | 220 |     |
| Ile | Gly | Gln | Val | Cys | Gly | Arg | Val | Thr | Pro | Thr | Phe | Glu | Ser | Ser | Ser | 225 | 230 | 235 | 240 |
| Asn | Ser | Leu | Thr | Val | Val | Leu | Ser | Thr | Asp | Tyr | Ala | Asn | Ser | Tyr | Arg | 245 | 250 | 255 |     |
| Gly | Phe | Ser | Ala | Ser | Tyr | Thr | Ser | Ile | Tyr | Ala | Glu | Asn | Ile | Asn | Thr | 260 | 265 | 270 |     |
| Thr | Ser | Leu | Thr | Cys | Ser | Ser | Asp | Arg | Met | Arg | Val | Ile | Ile | Ser | Lys | 275 | 280 | 285 |     |

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys  
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 305 310 315 320  
 Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile  
 325 330 335  
 Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val  
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 Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly  
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 His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile  
 370 375 380  
 Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe  
 385 390 395 400  
 Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val  
 405 410 415  
 Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp  
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 Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser  
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 Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg  
 450 455 460  
 Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe  
 465 470 475 480  
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 485 490 495  
 Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys  
 500 505 510  
 Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys  
 515 520 525  
 Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg  
 530 535 540  
 Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu  
 545 550 555 560  
 Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|     | 565 |     | 570 |     | 575 |     |     |     |     |     |     |     |     |     |     |
| Leu | Ala | Leu | Asn | Val | Val | Thr | Val | Ala | Thr | Ile | Thr | Val | Arg | His | Phe |
|     | 580 |     |     |     |     |     |     | 585 |     |     |     |     | 590 |     |     |
| Val | Asn | Gln | Arg | Ala | Asp | Tyr | Lys | Tyr | Gln | Lys | Leu | Gln | Asn | Tyr |     |
|     | 595 |     |     |     |     |     | 600 |     |     |     |     | 605 |     |     |     |

<210> 191  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 191  
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<210> 192  
 <211> 22  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 192  
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<210> 193  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 193  
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<210> 194  
 <211> 2362  
 <212> DNA  
 <213> Homo sapiens

<400> 194  
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<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

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Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala  
35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe  
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 Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro  
 85 90 95  
 Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe  
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 Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr  
 115 120 125  
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 130 135 140  
 Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp  
 145 150 155 160  
 Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg  
 165 170 175  
 Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu  
 180 185 190  
 Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys  
 195 200 205  
 Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val  
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 225 230 235 240  
 Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr  
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 Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly  
 260 265 270  
 Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro  
 275 280 285  
 His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr  
 290 295 300  
 Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val  
 305 310 315 320  
 Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn  
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg  
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Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr  
                   355                  360                  365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val  
                   370                  375                  380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu  
                   385                  390                  395                  400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile  
                   405                  410                  415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn  
                   420                  425                  430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu  
                   435                  440                  445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr  
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Asn Val Ile  
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 196

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23

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 198

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24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 199

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<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
                20                      25                      30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
    35                      40                      45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
    50                      55                      60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
    65                      70                      75                      80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
                85                      90                      95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
    100                      105                      110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
    115                      120                      125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
    130                      135                      140

```

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr  
 145 150 155 160  
 Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser  
 165 170 175  
 Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser  
 180 185 190  
 Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu  
 195 200 205  
 Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala  
 210 215 220  
 Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu  
 225 230 235 240  
 Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe  
 245 250 255  
 Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn  
 260 265 270  
 Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala  
 275 280 285  
 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro  
 290 295 300  
 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala  
 305 310 315 320  
 Glu Val

<210> 202

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 202

gagctttcca tccaggtgtc atgc

24

<210> 203

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 203

gtcagtgaca gtacctactc gg

22

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 204

tggagcagga ggagtagtag tagg

24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified\_base

<222> (973)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (977)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (996)

<223> a, t, c or g

<220>

<221> modified\_base

<222> (1003)

<223> a, t, c or g

<400> 206

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ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggt aaccctgtg 180
actttgactg gagagaagtg gagatcctga tgtttctcag tgccatttg atgatgaaga 240
accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
ccaacacaat tcttttcttc cgcttgata ttgcgatggg cctactttac atcacactct 360
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<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

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Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
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Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
      20                      25                      30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
      35                      40                      45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
      50                      55                      60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
      65                      70                      75                      80

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Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe  
                             85                            90                            95  
 Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met  
                             100                            105                            110  
 Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys  
                             115                            120                            125  
 Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys  
                             130                            135                            140  
 Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val  
  145                            150                            155                            160  
 Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile  
                             165                            170                            175  
 Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly  
                             180                            185                            190  
 Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val  
                             195                            200                            205  
 Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln  
                             210                            215                            220  
 Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg  
  225                            230                            235                            240  
 Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn  
                             245                            250                            255  
 Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp  
                             260                            265                            270  
 Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser  
                             275                            280                            285  
 Asp Gly Glu Asn Lys Lys Asp Lys  
                             290                            295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

<400> 208

gcttgatat tcgcatgggc ctac

<210> 209  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 209  
 tggagacaat atccctgagg 20

<210> 210  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 210  
 aacagttggc cacagcatgg cagg 24

<210> 211  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 211  
 ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag 50

<210> 212  
 <211> 1985  
 <212> DNA  
 <213> Homo sapiens

<400> 212  
 ggacagctcg cggcccccca gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60  
 tggggcccca gcctggcccg ggtcaccctg gcatgaggag atgggcctgt tgctcctggt 120  
 cccattgctc ctgctgcccg gctcctacgg actgcccttc tacaacggct tctactactc 180  
 caacagcgcc aacgaccaga acctaggcaa cggatcatgg aaagacctcc ttaatggagt 240  
 gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300  
 cctgccctgc cgtaccgct acgagccggc cctgggtctcc ccgcggcgtg tgcgtgtcaa 360  
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 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480  
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540  
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ctttccttac cagtccccca acgggcgcta ccagttcaac ttccacgagg gccagcaggt 660  
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 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcc 960  
 ggaagatgat gccacgatcg ccaagggtgg acagctcttt gccgcctgga agttccatgg 1020  
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980  
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met Gly Leu Leu Leu Val Pro Leu Leu Leu Leu Pro Gly Ser Tyr  
 1 5 10 15

Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp  
 20 25 30

Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys  
 35 40 45

Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala  
 50 55 60

Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser  
 65 70 75 80

Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala  
 85 90 95

Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe  
 100 105 110

Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp

| 115  | 120 | 125 |
|--|-----|-----|
| Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr<br>130 135 140     |     |     |
| Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu<br>145 150 155 160 |     |     |
| Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg<br>165 170 175     |     |     |
| Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala<br>180 185 190     |     |     |
| Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly<br>195 200 205     |     |     |
| Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr<br>210 215 220     |     |     |
| Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro<br>225 230 235 240 |     |     |
| Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp<br>245 250 255     |     |     |
| Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu<br>260 265 270     |     |     |
| His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu<br>275 280 285     |     |     |
| Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys<br>290 295 300     |     |     |
| Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser<br>305 310 315 320 |     |     |
| Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu<br>325 330 335     |     |     |
| Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr<br>340 345 350     |     |     |
| Gly Val Tyr Cys Tyr Arg Gln His<br>355 360   |     |     |

&lt;210&gt; 214

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;



&lt;210&gt; 219

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

&lt;400&gt; 219

gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag

45

&lt;210&gt; 220

&lt;211&gt; 1503

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 220

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ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gcttctgttg ctactgaggc acggggccca ggggaagcca tcccagacg caggccctca 120
tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctcccatg atgacgcca 180
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cgacgggcgt gtgggttggg aggagctgcg caacgccacc tatggccact acgcgcccgg 480
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cagctccaaa tctgagcctc caccacatag actgaaactc ccctggcccc agccctctcc 1380
tgcttggcct ggcctgggac acctcctctc tgccaggagg caataaaaagc cagcgccggg 1440
accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
aaa 1503

```

&lt;210&gt; 221

&lt;211&gt; 328

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

Met Met Trp Arg Pro Ser Val Leu Leu Leu Leu Leu Leu Arg His

|   |     |     |     |
|---|-----|-----|-----|
| 1   | 5   | 10  | 15  |
| Gly Ala Gln Gly Lys Pro Ser Pro Asp Ala Gly Pro His Gly Gln Gly | 20  | 25  | 30  |
| Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala | 35  | 40  | 45  |
| His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val | 50  | 55  | 60  |
| Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu | 65  | 70  | 75  |
| Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp | 85  | 90  | 95  |
| Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg | 100 | 105 | 110 |
| His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp | 115 | 120 | 125 |
| Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly | 130 | 135 | 140 |
| His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr | 145 | 150 | 155 |
| Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp | 165 | 170 | 175 |
| Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu | 180 | 185 | 190 |
| His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr | 195 | 200 | 205 |
| Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu | 210 | 215 | 220 |
| Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala | 225 | 230 | 235 |
| Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn | 245 | 250 | 255 |
| Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro | 260 | 265 | 270 |
| Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu | 275 | 280 | 285 |

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly  
 290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp  
 305 310 315 320

Leu Thr Arg His His Asp Glu Leu  
 325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe



&lt;400&gt; 225

ccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

&lt;210&gt; 226

&lt;211&gt; 2403

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 226

```

ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcggagcccc 60
gggcggcggg cgcgggtgcg agggatccct gacgcctctg tccctgtttc tttgtcgctc 120
ccagcctgtc tgtcgctcgtt ttggcgcccc cgccctcccc cggtgcgggg ttgcacaccg 180
atcctgggct tcgctcgatt tgccgcgcag gcgcctccca gacctagagg ggcgctggcc 240
tgagcagcgc ggtcgtctgt gtccctctct ctctgcgcgc cgcccgggga tccgaagggt 300
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ccatttcctt cactgttaga aatgtgtttg gccctataag ggagagcccc aacaagaact 1800
tcctagtaat tgtcacagat gggcagtcct atgatgatgt ccaaggccct gcagctgctg 1860
cacatgatgc aggaatcact atcttctctg ttggtgtggc ttgggcacct ctggatgacc 1920
tgaaagatat ggcttctaaa ccgaaggagt ctacgcctt cttcacaaga gatttcacag 1980
gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
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attgtattct cataatactg aaatgcttta gcatactaga atcagataca aaactattaa 2160
gtatgtcaac agccatttag gcaaataagc actcctttaa agccgctgcc ttctggttac 2220
aatttacagt gtactttgtt aaaaacactg ctgaggcttc ataactatgg ctcttagaaa 2280
ctcaggaaag aggagataat gtggattaaa accttaagag ttctaaccat gctactaaa 2340
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aaa
2403

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&lt;210&gt; 227



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 290 295 300  
 Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys  
 305 310 315 320  
 Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp  
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 Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr  
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 His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile  
 355 360 365  
 Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg  
 370 375 380  
 Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser  
 385 390 395 400  
 Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg  
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 Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala  
 420 425 430  
 Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp  
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 Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser  
 450 455 460  
 Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp  
 465 470 475 480  
 Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile  
 485 490 495  
 Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met  
 500 505 510  
 Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr  
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Phe Leu Glu Ser Gln Gln  
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<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide probe

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18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<400> 229

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18

<210> 230

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<400> 230

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<210> 231

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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<210> 232

<211> 18  
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<223> Description of Artificial Sequence: Synthetic  
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<223> Description of Artificial Sequence: Synthetic  
 oligonucleotide probe

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<210> 234  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
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<210> 235  
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 <213> Homo sapiens

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 gcctgctgct ggcggcgcg gtccccacgg ccccgcgcc cgctccgacg gcgacctcg 240  
 ctccagtcaa gcccggccc gctctcagct acccgagga ggaggccacc ctcaatgaga 300  
 tgttccgcga gggtgaggaa ctgatggagg acacgcagca caaattgagc agcgcggtgg 360  
 aagagatgga ggcagaagaa gctgctgcta aagcatcatc agaagtgaac ctggcaaact 420  
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaat aataccatcc 480  
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 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcattcatcg 600  
 acgaggactg tggggccagc atgtactgcc agtttgccag cttccagtac acctgccagc 660  
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gtgtctgggg tcaactgcacc aaaatggcca ccaggggcag caatgggacc atctgtgaca 780
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aagttgcatt tagaaatcaa gcataaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
aaaaaa 2586

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&lt;210&gt; 236

&lt;211&gt; 350

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 236

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Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
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Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
      20              25              30

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
      35              40              45

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Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
      65              70              75              80

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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn  
                             85                            90                            95  
 Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His  
                             100                            105                            110  
 Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe  
                             115                            120                            125  
 Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser  
                             130                            135                            140  
 His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln  
                             145                            150                            155                            160  
 Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met  
                             165                            170                            175  
 Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp  
                             180                            185                            190  
 Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys  
                             195                            200                            205  
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 Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu  
                             225                            230                            235                            240  
 Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu  
                             245                            250                            255  
 Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu  
                             260                            265                            270  
 Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe  
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 Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val  
                             290                            295                            300  
 Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu  
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 Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu  
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&lt;210&gt; 237

<211> 17  
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<220>  
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<400> 237  
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<210> 238  
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 <212> DNA  
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<220>  
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<400> 238  
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<400> 239  
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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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| Met | Arg | Leu | Leu | Val | Ala | Pro | Leu | Leu | Leu | Ala | Trp | Val | Ala | Gly |
| 1   |     |     |     | 5   |     |     |     |     |     | 10  |     |     |     | 15  |
| Ala | Thr | Ala | Thr | Val | Pro | Val | Val | Pro | Trp | His | Val | Pro | Cys | Pro |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Pro | Gln | Cys | Ala | Cys | Gln | Ile | Arg | Pro | Trp | Tyr | Thr | Pro | Arg | Ser |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Ser | Tyr | Arg | Glu | Ala | Thr | Thr | Val | Asp | Cys | Asn | Asp | Leu | Phe | Leu |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Thr | Ala | Val | Pro | Pro | Ala | Leu | Pro | Ala | Gly | Thr | Gln | Thr | Leu | Leu |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Leu | Gln | Ser | Asn | Ser | Ile | Val | Arg | Val | Asp | Gln | Ser | Glu | Leu | Gly |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Tyr | Leu | Ala | Asn | Leu | Thr | Glu | Leu | Asp | Leu | Ser | Gln | Asn | Ser | Phe |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Ser | Asp | Ala | Arg | Asp | Cys | Asp | Phe | His | Ala | Leu | Pro | Gln | Leu | Leu |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Ser | Leu | His | Leu | Glu | Glu | Asn | Gln | Leu | Thr | Arg | Leu | Glu | Asp | His |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Ser | Phe | Ala | Gly | Leu | Ala | Ser | Leu | Gln | Glu | Leu | Tyr | Leu | Asn | His |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |

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|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Asn | Gln | Leu | Tyr | Arg<br>155 | Ile | Ala | Pro | Arg | Ala<br>160 | Phe | Ser | Gly | Leu | Ser<br>165 |
| Asn | Leu | Leu | Arg | Leu<br>170 | His | Leu | Asn | Ser | Asn<br>175 | Leu | Leu | Arg | Ala | Ile<br>180 |
| Asp | Ser | Arg | Trp | Phe<br>185 | Glu | Met | Leu | Pro | Asn<br>190 | Leu | Glu | Ile | Leu | Met<br>195 |
| Ile | Gly | Gly | Asn | Lys<br>200 | Val | Asp | Ala | Ile | Leu<br>205 | Asp | Met | Asn | Phe | Arg<br>210 |
| Pro | Leu | Ala | Asn | Leu<br>215 | Arg | Ser | Leu | Val | Leu<br>220 | Ala | Gly | Met | Asn | Leu<br>225 |
| Arg | Glu | Ile | Ser | Asp<br>230 | Tyr | Ala | Leu | Glu | Gly<br>235 | Leu | Gln | Ser | Leu | Glu<br>240 |
| Ser | Leu | Ser | Phe | Tyr<br>245 | Asp | Asn | Gln | Leu | Ala<br>250 | Arg | Val | Pro | Arg | Arg<br>255 |
| Ala | Leu | Glu | Gln | Val<br>260 | Pro | Gly | Leu | Lys | Phe<br>265 | Leu | Asp | Leu | Asn | Lys<br>270 |
| Asn | Pro | Leu | Gln | Arg<br>275 | Val | Gly | Pro | Gly | Asp<br>280 | Phe | Ala | Asn | Met | Leu<br>285 |
| His | Leu | Lys | Glu | Leu<br>290 | Gly | Leu | Asn | Asn | Met<br>295 | Glu | Glu | Leu | Val | Ser<br>300 |
| Ile | Asp | Lys | Phe | Ala<br>305 | Leu | Val | Asn | Leu | Pro<br>310 | Glu | Leu | Thr | Lys | Leu<br>315 |
| Asp | Ile | Thr | Asn | Asn<br>320 | Pro | Arg | Leu | Ser | Phe<br>325 | Ile | His | Pro | Arg | Ala<br>330 |
| Phe | His | His | Leu | Pro<br>335 | Gln | Met | Glu | Thr | Leu<br>340 | Met | Leu | Asn | Asn | Asn<br>345 |
| Ala | Leu | Ser | Ala | Leu<br>350 | His | Gln | Gln | Thr | Val<br>355 | Glu | Ser | Leu | Pro | Asn<br>360 |
| Leu | Gln | Glu | Val | Gly<br>365 | Leu | His | Gly | Asn | Pro<br>370 | Ile | Arg | Cys | Asp | Cys<br>375 |
| Val | Ile | Arg | Trp | Ala<br>380 | Asn | Ala | Thr | Gly | Thr<br>385 | Arg | Val | Arg | Phe | Ile<br>390 |
| Glu | Pro | Gln | Ser | Thr<br>395 | Leu | Cys | Ala | Glu | Pro<br>400 | Pro | Asp | Leu | Gln | Arg<br>405 |
| Leu | Pro | Val | Arg | Glu        | Val | Pro | Phe | Arg | Glu        | Met | Thr | Asp | His | Cys        |

|                 | 410                 |                         | 415 |  | 420 |
|-----------------|---------------------|-------------------------|-----|--|-----|
| Leu Pro Leu Ile | Ser Pro Arg Ser Phe | Pro Pro Ser Leu Gln Val |     |  |     |
|                 | 425                 |                         | 430 |  | 435 |
| Ala Ser Gly Glu | Ser Met Val Leu His | Cys Arg Ala Leu Ala Glu |     |  |     |
|                 | 440                 |                         | 445 |  | 450 |
| Pro Glu Pro Glu | Ile Tyr Trp Val Thr | Pro Ala Gly Leu Arg Leu |     |  |     |
|                 | 455                 |                         | 460 |  | 465 |
| Thr Pro Ala His | Ala Gly Arg Arg Tyr | Arg Val Tyr Pro Glu Gly |     |  |     |
|                 | 470                 |                         | 475 |  | 480 |
| Thr Leu Glu Leu | Arg Arg Val Thr Ala | Glu Glu Ala Gly Leu Tyr |     |  |     |
|                 | 485                 |                         | 490 |  | 495 |
| Thr Cys Val Ala | Gln Asn Leu Val Gly | Ala Asp Thr Lys Thr Val |     |  |     |
|                 | 500                 |                         | 505 |  | 510 |
| Ser Val Val Val | Gly Arg Ala Leu Leu | Gln Pro Gly Arg Asp Glu |     |  |     |
|                 | 515                 |                         | 520 |  | 525 |
| Gly Gln Gly Leu | Glu Leu Arg Val Gln | Glu Thr His Pro Tyr His |     |  |     |
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| Ile Leu Leu Ser | Trp Val Thr Pro Pro | Asn Thr Val Ser Thr Asn |     |  |     |
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| Leu Thr Trp Ser | Ser Ala Ser Ser Leu | Arg Gly Gln Gly Ala Thr |     |  |     |
|                 | 560                 |                         | 565 |  | 570 |
| Ala Leu Ala Arg | Leu Pro Arg Gly Thr | His Ser Tyr Asn Ile Thr |     |  |     |
|                 | 575                 |                         | 580 |  | 585 |
| Arg Leu Leu Gln | Ala Thr Glu Tyr Trp | Ala Cys Leu Gln Val Ala |     |  |     |
|                 | 590                 |                         | 595 |  | 600 |
| Phe Ala Asp Ala | His Thr Gln Leu Ala | Cys Val Trp Ala Arg Thr |     |  |     |
|                 | 605                 |                         | 610 |  | 615 |
| Lys Glu Ala Thr | Ser Cys His Arg Ala | Leu Gly Asp Arg Pro Gly |     |  |     |
|                 | 620                 |                         | 625 |  | 630 |
| Leu Ile Ala Ile | Leu Ala Leu Ala Val | Leu Leu Leu Ala Ala Gly |     |  |     |
|                 | 635                 |                         | 640 |  | 645 |
| Leu Ala Ala His | Leu Gly Thr Gly Gln | Pro Arg Lys Gly Val Gly |     |  |     |
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147





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<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Gln | Thr | Ile | Ile | Lys | Val | Ile | Lys | Phe | Ile | Leu | Ile | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Tyr | Thr | Val | Tyr | Tyr | Val | His | Asn | Ile | Lys | Phe | Asp | Val | Asp |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Thr | Val | Asp | Ile | Glu | Ser | Leu | Thr | Gly | Tyr | Arg | Thr | Tyr | Arg |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | His | Pro | Leu | Ala | Thr | Leu | Phe | Lys | Ile | Leu | Ala | Ser | Phe |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Ser | Leu | Val | Ile | Phe | Tyr | Gly | Leu | Ile | Cys | Met | Tyr | Thr |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Trp | Trp | Met | Leu | Arg | Arg | Ser | Leu | Lys | Lys | Tyr | Ser | Phe | Glu |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Ile | Arg | Glu | Glu | Ser | Ser | Tyr | Ser | Asp | Ile | Pro | Asp | Val | Lys |
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|   | 95  | 100 | 105 |
|---|-----|-----|-----|
| Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro | 110 | 115 | 120 |
| Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu | 125 | 130 | 135 |
| Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp | 140 | 145 | 150 |
| Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu | 155 | 160 | 165 |
| Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp | 170 | 175 | 180 |
| Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val | 185 | 190 | 195 |
| Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu | 200 | 205 | 210 |
| Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala | 215 | 220 | 225 |
| Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp | 230 | 235 | 240 |
| Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu | 245 | 250 | 255 |
| Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr | 260 | 265 | 270 |
| Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu | 275 | 280 | 285 |
| Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp | 290 | 295 | 300 |
| Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr | 305 | 310 | 315 |
| Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr | 320 | 325 | 330 |
| Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser | 335 | 340 | 345 |
| Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn | 350 | 355 | 360 |

1000 900 800 700 600 500 400 300 200 100 0

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Lys | Thr | Ile | Glu | Glu | Ile | Ile | Ser | Phe | Gln | His | Leu | His |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |
| Arg | Leu | Thr | Cys | Leu | Lys | Leu | Trp | Tyr | Asn | His | Ile | Ala | Tyr | Ile |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |
| Pro | Ile | Gln | Ile | Gly | Asn | Leu | Thr | Asn | Leu | Glu | Arg | Leu | Tyr | Leu |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |
| Asn | Arg | Asn | Lys | Ile | Glu | Lys | Ile | Pro | Thr | Gln | Leu | Phe | Tyr | Cys |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |
| Arg | Lys | Leu | Arg | Tyr | Leu | Asp | Leu | Ser | His | Asn | Asn | Leu | Thr | Phe |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |
| Leu | Pro | Ala | Asp | Ile | Gly | Leu | Leu | Gln | Asn | Leu | Gln | Asn | Leu | Ala |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |
| Ile | Thr | Ala | Asn | Arg | Ile | Glu | Thr | Leu | Pro | Pro | Glu | Leu | Phe | Gln |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |
| Cys | Arg | Lys | Leu | Arg | Ala | Leu | His | Leu | Gly | Asn | Asn | Val | Leu | Gln |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Ser | Leu | Pro | Ser | Arg | Val | Gly | Glu | Leu | Thr | Asn | Leu | Thr | Gln | Ile |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |
| Glu | Leu | Arg | Gly | Asn | Arg | Leu | Glu | Cys | Leu | Pro | Val | Glu | Leu | Gly |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |
| Glu | Cys | Pro | Leu | Leu | Lys | Arg | Ser | Gly | Leu | Val | Val | Glu | Glu | Asp |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |
| Leu | Phe | Asn | Thr | Leu | Pro | Pro | Glu | Val | Lys | Glu | Arg | Leu | Trp | Arg |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |
| Ala | Asp | Lys | Glu | Gln | Ala |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 545 |     |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 251

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 251

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&lt;210&gt; 252

&lt;211&gt; 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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tgaacgcagg agctgtcatt gactggccca cagaggaggg caaggaagta 150  
tgggattatg tgacgggtccg caaggatgcc tacatgttct ggtggctcta 200  
ttatgccacc aactcctgca agaacttctc agaactgccc ctggtcattgt 250  
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gaaattgggc cccttgacag tgatctcaaa ccacggaaaa ccacctggct 350  
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ccagacagtt ccattctaca ttttctcaga gtccatgga ggaaaaatgg 550  
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ggaggcaatt tggaaattat ttctgcttct taaaaaaacc taagattttt 1600  
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ala | Leu | Arg | Arg | Ser | Pro | Val | Pro | Arg | Trp | Leu | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |
| Leu | Leu | Pro | Leu | Leu | Leu | Gly | Leu | Asn | Ala | Gly | Ala | Val | Ile | Asp |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |
| Trp | Pro | Thr | Glu | Glu | Gly | Lys | Glu | Val | Trp | Asp | Tyr | Val | Thr | Val |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Lys | Asp | Ala | Tyr | Met | Phe | Trp | Trp | Leu | Tyr | Tyr | Ala | Thr | Asn | 50  | 55  | 60  |
| Ser | Cys | Lys | Asn | Phe | Ser | Glu | Leu | Pro | Leu | Val | Met | Trp | Leu | Gln | 65  | 70  | 75  |
| Gly | Gly | Pro | Gly | Gly | Ser | Ser | Thr | Gly | Phe | Gly | Asn | Phe | Glu | Glu | 80  | 85  | 90  |
| Ile | Gly | Pro | Leu | Asp | Ser | Asp | Leu | Lys | Pro | Arg | Lys | Thr | Thr | Trp | 95  | 100 | 105 |
| Leu | Gln | Ala | Ala | Ser | Leu | Leu | Phe | Val | Asp | Asn | Pro | Val | Gly | Thr | 110 | 115 | 120 |
| Gly | Phe | Ser | Tyr | Val | Asn | Gly | Ser | Gly | Ala | Tyr | Ala | Lys | Asp | Leu | 125 | 130 | 135 |
| Ala | Met | Val | Ala | Ser | Asp | Met | Met | Val | Leu | Leu | Lys | Thr | Phe | Phe | 140 | 145 | 150 |
| Ser | Cys | His | Lys | Glu | Phe | Gln | Thr | Val | Pro | Phe | Tyr | Ile | Phe | Ser | 155 | 160 | 165 |
| Glu | Ser | Tyr | Gly | Gly | Lys | Met | Ala | Ala | Gly | Ile | Gly | Leu | Glu | Leu | 170 | 175 | 180 |
| Tyr | Lys | Ala | Ile | Gln | Arg | Gly | Thr | Ile | Lys | Cys | Asn | Phe | Ala | Gly | 185 | 190 | 195 |
| Val | Ala | Leu | Gly | Asp | Ser | Trp | Ile | Ser | Pro | Val | Asp | Ser | Val | Leu | 200 | 205 | 210 |
| Ser | Trp | Gly | Pro | Tyr | Leu | Tyr | Ser | Met | Ser | Leu | Leu | Glu | Asp | Lys | 215 | 220 | 225 |
| Gly | Leu | Ala | Glu | Val | Ser | Lys | Val | Ala | Glu | Gln | Val | Leu | Asn | Ala | 230 | 235 | 240 |
| Val | Asn | Lys | Gly | Leu | Tyr | Arg | Glu | Ala | Thr | Glu | Leu | Trp | Gly | Lys | 245 | 250 | 255 |
| Ala | Glu | Met | Ile | Ile | Glu | Gln | Asn | Thr | Asp | Gly | Val | Asn | Phe | Tyr | 260 | 265 | 270 |
| Asn | Ile | Leu | Thr | Lys | Ser | Thr | Pro | Thr | Ser | Thr | Met | Glu | Ser | Ser | 275 | 280 | 285 |
| Leu | Glu | Phe | Thr | Gln | Ser | His | Leu | Val | Cys | Leu | Cys | Gln | Arg | His | 290 | 295 | 300 |
| Val | Arg | His | Leu | Gln | Arg | Asp | Ala | Leu | Ser | Gln | Leu | Met | Asn | Gly |     |     |     |

| 305                                 | 310                     | 315 |
|-------------------------------------|-------------------------|-----|
| Pro Ile Arg Lys Lys Leu Lys Ile Ile | Pro Glu Asp Gln Ser Trp |     |
| 320                                 | 325                     | 330 |
| Gly Gly Gln Ala Thr Asn Val Phe Val | Asn Met Glu Glu Asp Phe |     |
| 335                                 | 340                     | 345 |
| Met Lys Pro Val Ile Ser Ile Val Asp | Glu Leu Leu Glu Ala Gly |     |
| 350                                 | 355                     | 360 |
| Ile Asn Val Thr Val Tyr Asn Gly Gln | Leu Asp Leu Ile Val Asp |     |
| 365                                 | 370                     | 375 |
| Thr Met Gly Gln Glu Ala Trp Val Arg | Lys Leu Lys Trp Pro Glu |     |
| 380                                 | 385                     | 390 |
| Leu Pro Lys Phe Ser Gln Leu Lys Trp | Lys Ala Leu Tyr Ser Asp |     |
| 395                                 | 400                     | 405 |
| Pro Lys Ser Leu Glu Thr Ser Ala Phe | Val Lys Ser Tyr Lys Asn |     |
| 410                                 | 415                     | 420 |
| Leu Ala Phe Tyr Trp Ile Leu Lys Ala | Gly His Met Val Pro Ser |     |
| 425                                 | 430                     | 435 |
| Asp Gln Gly Asp Met Ala Leu Lys Met | Met Arg Leu Val Thr Gln |     |
| 440                                 | 445                     | 450 |

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200
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ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300
cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400

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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ala | Arg | Gly | Ala | Leu | Leu | Leu | Ala | Leu | Leu | Leu | Ala | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Leu | Arg | Lys | Pro | Glu | Ser | Gln | Glu | Ala | Ala | Pro | Leu | Ser |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     | 30  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Pro | Cys | Gly | Arg | Arg | Val | Ile | Thr | Ser | Arg | Ile | Val | Gly | Gly |
|     |     |     | 35  |     |     |     |     |     | 40  |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Ala | Glu | Leu | Gly | Arg | Trp | Pro | Trp | Gln | Gly | Ser | Leu | Arg |
|     |     |     | 50  |     |     |     |     |     | 55  |     |     |     | 60  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Trp | Asp | Ser | His | Val | Cys | Gly | Val | Ser | Leu | Leu | Ser | His | Arg |
|     |     |     | 65  |     |     |     |     |     | 70  |     |     |     | 75  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Leu | Thr | Ala | Ala | His | Cys | Phe | Glu | Thr | Tyr | Ser | Asp | Leu |
|     |     |     | 80  |     |     |     |     |     | 85  |     |     |     | 90  |     |

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser  
 95 100 105  
 Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe  
 110 115 120  
 Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro  
 125 130 135  
 Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr  
 140 145 150  
 Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe  
 155 160 165  
 Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys  
 170 175 180  
 Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln  
 185 190 195  
 Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys  
 200 205 210  
 Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly  
 215 220 225  
 Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly  
 230 235 240  
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val  
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 Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val  
 260 265 270  
 Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met  
 275 280 285  
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&lt;210&gt; 258

&lt;211&gt; 2427

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 258

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100 150 200 250 300 350 400 450 500 550 600 650 700 750 800 850 900 950 1000 1050 1100 1150 1200 1250 1300 1350 1400



[illegible]

|                 |                     |                         |     |     |     |
|-----------------|---------------------|-------------------------|-----|-----|-----|
| Asn Ile Ser Thr | Trp Val Tyr Ser Ser | Pro Gly Arg His Glu Gly | 290 | 295 | 300 |
| Gln Glu Pro Phe | Leu Gln Trp Leu Met | Leu Leu Ser Asn Glu Ser | 305 | 310 | 315 |
| Ala Leu Pro His | Val His Thr Val Ser | Tyr Gly Asp Asp Glu Asp | 320 | 325 | 330 |
| Ser Leu Ser Ser | Ala Tyr Ile Gln Arg | Val Asn Thr Glu Leu Met | 335 | 340 | 345 |
| Lys Ala Ala Ala | Arg Gly Leu Thr Leu | Leu Phe Ala Ser Gly Asp | 350 | 355 | 360 |
| Ser Gly Ala Gly | Cys Trp Ser Val Ser | Gly Arg His Gln Phe Arg | 365 | 370 | 375 |
| Pro Thr Phe Pro | Ala Ser Ser Pro Tyr | Val Thr Thr Val Gly Gly | 380 | 385 | 390 |
| Thr Ser Phe Gln | Glu Pro Phe Leu Ile | Thr Asn Glu Ile Val Asp | 395 | 400 | 405 |
| Tyr Ile Ser Gly | Gly Gly Phe Ser Asn | Val Phe Pro Arg Pro Ser | 410 | 415 | 420 |
| Tyr Gln Glu Glu | Ala Val Thr Lys Phe | Leu Ser Ser Ser Pro His | 425 | 430 | 435 |
| Leu Pro Pro Ser | Ser Tyr Phe Asn Ala | Ser Gly Arg Ala Tyr Pro | 440 | 445 | 450 |
| Asp Val Ala Ala | Leu Ser Asp Gly Tyr | Trp Val Val Ser Asn Arg | 455 | 460 | 465 |
| Val Pro Ile Pro | Trp Val Ser Gly Thr | Ser Ala Ser Thr Pro Val | 470 | 475 | 480 |
| Phe Gly Gly Ile | Leu Ser Leu Ile Asn | Glu His Arg Ile Leu Ser | 485 | 490 | 495 |
| Gly Arg Pro Pro | Leu Gly Phe Leu Asn | Pro Arg Leu Tyr Gln Gln | 500 | 505 | 510 |
| His Gly Ala Gly | Leu Phe Asp Val Thr | Arg Gly Cys His Glu Ser | 515 | 520 | 525 |
| Cys Leu Asp Glu | Glu Val Glu Gly Gln | Gly Phe Cys Ser Gly Pro | 530 | 535 | 540 |
| Gly Trp Asp Pro | Val Thr Gly Trp Gly | Thr Pro Thr Ser Gln Leu | 545 | 550 | 555 |

Cys

&lt;210&gt; 260

&lt;211&gt; 1638

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 260

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1100 1050 1000 950 900 850 800 750 700 650 600 550 500 450 400 350 300 250 200 150 100 50





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 Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe  
 140 145 150  
 Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val  
 155 160 165  
 Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly  
 170 175 180  
 Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu  
 185 190 195  
 Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr  
 200 205 210  
 Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys  
 215 220 225  
 Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp  
 230 235 240  
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro  
 245 250 255  
 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys  
 260 265 270  
 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp  
 275 280 285  
 Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu  
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 320 325 330  
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 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg  
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 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly  
 365 370 375  
 Asn Tyr Leu Asp Cys Arg Glu Gly  
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<211> 317

<212> PRT

<213> Homo Sapien.

<400> 263

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| Met | Val | Val | Ser | Gly | Ala | Pro | Pro | Ala | Leu | Gly | Gly | Gly | Cys | Leu | 1   | 5   | 10  | 15 |
| Gly | Thr | Phe | Thr | Ser | Leu | Leu | Leu | Leu | Ala | Ser | Thr | Ala | Ile | Leu | 20  | 25  | 30  |    |
| Asn | Ala | Ala | Arg | Ile | Pro | Val | Pro | Pro | Ala | Cys | Gly | Lys | Pro | Gln | 35  | 40  | 45  |    |
| Gln | Leu | Asn | Arg | Val | Val | Gly | Gly | Glu | Asp | Ser | Thr | Asp | Ser | Glu | 50  | 55  | 60  |    |
| Trp | Pro | Trp | Ile | Val | Ser | Ile | Gln | Lys | Asn | Gly | Thr | His | His | Cys | 65  | 70  | 75  |    |
| Ala | Gly | Ser | Leu | Leu | Thr | Ser | Arg | Trp | Val | Ile | Thr | Ala | Ala | His | 80  | 85  | 90  |    |
| Cys | Phe | Lys | Asp | Asn | Leu | Asn | Lys | Pro | Tyr | Leu | Phe | Ser | Val | Leu | 95  | 100 | 105 |    |
| Leu | Gly | Ala | Trp | Gln | Leu | Gly | Asn | Pro | Gly | Ser | Arg | Ser | Gln | Lys | 110 | 115 | 120 |    |
| Val | Gly | Val | Ala | Trp | Val | Glu | Pro | His | Pro | Val | Tyr | Ser | Trp | Lys | 125 | 130 | 135 |    |
| Glu | Gly | Ala | Cys | Ala | Asp | Ile | Ala | Leu | Val | Arg | Leu | Glu | Arg | Ser | 140 | 145 | 150 |    |
| Ile | Gln | Phe | Ser | Glu | Arg | Val | Leu | Pro | Ile | Cys | Leu | Pro | Asp | Ala | 155 | 160 | 165 |    |
| Ser | Ile | His | Leu | Pro | Pro | Asn | Thr | His | Cys | Trp | Ile | Ser | Gly | Trp | 170 | 175 | 180 |    |

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<213> Artificial Sequence

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<211> 19

<213> Artificial Sequence

### <223> Synthetic Oligonucleotide Probe

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<211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
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<210> 267  
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<212> DNA

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FILE 1720 00000000





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<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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| Met | His | Gly | Ser | Cys | Ser | Phe | Leu | Met | Leu | Leu | Leu | Pro | Leu | Leu |  |  |  |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |  |  |  |  |  |
| Leu | Leu | Leu | Val | Ala | Thr | Thr | Gly | Pro | Val | Gly | Ala | Leu | Thr | Asp |  |  |  |  |  |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |  |  |  |  |  |
| Glu | Glu | Lys | Arg | Leu | Met | Val | Glu | Leu | His | Asn | Leu | Tyr | Arg | Ala |  |  |  |  |  |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |  |  |  |  |  |
| Gln | Val | Ser | Pro | Thr | Ala | Ser | Asp | Met | Leu | His | Met | Arg | Trp | Asp |  |  |  |  |  |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |  |  |  |  |  |
| Glu | Glu | Leu | Ala | Ala | Phe | Ala | Lys | Ala | Tyr | Ala | Arg | Gln | Cys | Val |  |  |  |  |  |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |  |  |  |  |  |
| Trp | Gly | His | Asn | Lys | Glu | Arg | Gly | Arg | Arg | Gly | Glu | Asn | Leu | Phe |  |  |  |  |  |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |  |  |  |  |  |
| Ala | Ile | Thr | Asp | Glu | Gly | Met | Asp | Val | Pro | Leu | Ala | Met | Glu | Glu |  |  |  |  |  |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |  |  |  |  |  |
| Trp | His | His | Glu | Arg | Glu | His | Tyr | Asn | Leu | Ser | Ala | Ala | Thr | Cys |  |  |  |  |  |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |  |  |  |  |  |
| Ser | Pro | Gly | Gln | Met | Cys | Gly | His | Tyr | Thr | Gln | Val | Val | Trp | Ala |  |  |  |  |  |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |  |  |  |  |  |



Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser  
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser  
425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly  
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Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe  
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<211> 3662

<212> DNA

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176

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<212> PRT

<213> Homo Sapien

<400> 290

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Val | Leu | Leu | Leu | Phe | Ser | Leu | Cys | Leu | Leu | Phe | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ser | Arg | Pro | Asp | Leu | Ser | His | Asn | Arg | Leu | Ser | Phe | Ile | Lys |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |





|     |     |     |     |            |     |     |     |     |     |     |     |     |     |            |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------------|
|     |     |     |     | 290        |     |     |     |     | 295 |     |     |     |     | 300        |
| Leu | Lys | Thr | Leu | Asp<br>305 | Leu | Lys | Asn | Asn | Glu | Ile | Ser | Trp | Thr | Ile<br>315 |
| Glu | Asp | Met | Asn | Gly<br>320 | Ala | Phe | Ser | Gly | Leu | Asp | Lys | Leu | Arg | Arg<br>330 |
| Leu | Ile | Leu | Gln | Gly<br>335 | Asn | Arg | Ile | Arg | Ser | Ile | Thr | Lys | Lys | Ala<br>345 |
| Phe | Thr | Gly | Leu | Asp<br>350 | Ala | Leu | Glu | His | Leu | Asp | Leu | Ser | Asp | Asn<br>360 |
| Ala | Ile | Met | Ser | Leu<br>365 | Gln | Gly | Asn | Ala | Phe | Ser | Gln | Met | Lys | Lys<br>375 |
| Leu | Gln | Gln | Leu | His<br>380 | Leu | Asn | Thr | Ser | Ser | Leu | Leu | Cys | Asp | Cys<br>390 |
| Gln | Leu | Lys | Trp | Leu<br>395 | Pro | Gln | Trp | Val | Ala | Glu | Asn | Asn | Phe | Gln<br>405 |
| Ser | Phe | Val | Asn | Ala<br>410 | Ser | Cys | Ala | His | Pro | Gln | Leu | Leu | Lys | Gly<br>420 |
| Arg | Ser | Ile | Phe | Ala<br>425 | Val | Ser | Pro | Asp | Gly | Phe | Val | Cys | Asp | Asp<br>435 |
| Phe | Pro | Lys | Pro | Gln<br>440 | Ile | Thr | Val | Gln | Pro | Glu | Thr | Gln | Ser | Ala<br>450 |
| Ile | Lys | Gly | Ser | Asn<br>455 | Leu | Ser | Phe | Ile | Cys | Ser | Ala | Ala | Ser | Ser<br>465 |
| Ser | Asp | Ser | Pro | Met<br>470 | Thr | Phe | Ala | Trp | Lys | Lys | Asp | Asn | Glu | Leu<br>480 |
| Leu | His | Asp | Ala | Glu<br>485 | Met | Glu | Asn | Tyr | Ala | His | Leu | Arg | Ala | Gln<br>495 |
| Gly | Gly | Glu | Val | Met<br>500 | Glu | Tyr | Thr | Thr | Ile | Leu | Arg | Leu | Arg | Glu<br>510 |
| Val | Glu | Phe | Ala | Ser<br>515 | Glu | Gly | Lys | Tyr | Gln | Cys | Val | Ile | Ser | Asn<br>525 |
| His | Phe | Gly | Ser | Ser<br>530 | Tyr | Ser | Val | Lys | Ala | Lys | Leu | Thr | Val | Asn<br>540 |
| Met | Leu | Pro | Ser | Phe<br>545 | Thr | Lys | Thr | Pro | Met | Asp | Leu | Thr | Ile | Arg<br>555 |



Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser  
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 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr  
 830 835 840  
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr  
 845 850 855  
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr  
 860 865 870  
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His  
 875 880 885  
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr  
 890 895 900  
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His  
 905 910 915  
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp  
 920 925 930  
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn  
 935 940 945  
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu  
 950 955 960  
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn  
 965 970 975  
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu  
 980 985 990  
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg  
 995 1000 1005  
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly  
 1010 1015 1020  
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn  
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 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  
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 Asn Phe Gln Ser Tyr Asp Leu Asp Thr  
 1055

&lt;210&gt; 291

&lt;211&gt; 2906

 0000438 074301  
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<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Asn | Lys | Met | Thr | Leu | His | Pro | Gln | Gln | Ile | Met | Ile | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Pro | Arg | Phe | Asn | Arg | Ala | Leu | Phe | Asp | Pro | Leu | Leu | Val | Val | Leu |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Leu | Ala | Leu | Gln | Leu | Leu | Val | Val | Ala | Gly | Leu | Val | Arg | Ala | Gln |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Thr | Cys | Pro | Ser | Val | Cys | Ser | Cys | Ser | Asn | Gln | Phe | Ser | Lys | Val |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Ile | Cys | Val | Arg | Lys | Asn | Leu | Arg | Glu | Val | Pro | Asp | Gly | Ile | Ser |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Thr | Asn | Thr | Arg | Leu | Leu | Asn | Leu | His | Glu | Asn | Gln | Ile | Gln | Ile |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Ile | Lys | Val | Asn | Ser | Phe | Lys | His | Leu | Arg | His | Leu | Glu | Ile | Leu |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Gln | Leu | Ser | Arg | Asn | His | Ile | Arg | Thr | Ile | Glu | Ile | Gly | Ala | Phe |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Asn | Gly | Leu | Ala | Asn | Leu | Asn | Thr | Leu | Glu | Leu | Phe | Asp | Asn | Arg |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Leu | Thr | Thr | Ile | Pro | Asn | Gly | Ala | Phe | Val | Tyr | Leu | Ser | Lys | Leu |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Lys | Glu | Leu | Trp | Leu | Arg | Asn | Asn | Pro | Ile | Glu | Ser | Ile | Pro | Ser |

|     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
|     |     |     |     | 155        |     |     |     |     | 160        |     |     |     |     | 165        |
| Tyr | Ala | Phe | Asn | Arg<br>170 | Ile | Pro | Ser | Leu | Arg<br>175 | Arg | Leu | Asp | Leu | Gly<br>180 |
| Glu | Leu | Lys | Arg | Leu<br>185 | Ser | Tyr | Ile | Ser | Glu<br>190 | Gly | Ala | Phe | Glu | Gly<br>195 |
| Leu | Ser | Asn | Leu | Arg<br>200 | Tyr | Leu | Asn | Leu | Ala<br>205 | Met | Cys | Asn | Leu | Arg<br>210 |
| Glu | Ile | Pro | Asn | Leu<br>215 | Thr | Pro | Leu | Ile | Lys<br>220 | Leu | Asp | Glu | Leu | Asp<br>225 |
| Leu | Ser | Gly | Asn | His<br>230 | Leu | Ser | Ala | Ile | Arg<br>235 | Pro | Gly | Ser | Phe | Gln<br>240 |
| Gly | Leu | Met | His | Leu<br>245 | Gln | Lys | Leu | Trp | Met<br>250 | Ile | Gln | Ser | Gln | Ile<br>255 |
| Gln | Val | Ile | Glu | Arg<br>260 | Asn | Ala | Phe | Asp | Asn<br>265 | Leu | Gln | Ser | Leu | Val<br>270 |
| Glu | Ile | Asn | Leu | Ala<br>275 | His | Asn | Asn | Leu | Thr<br>280 | Leu | Leu | Pro | His | Asp<br>285 |
| Leu | Phe | Thr | Pro | Leu<br>290 | His | His | Leu | Glu | Arg<br>295 | Ile | His | Leu | His | His<br>300 |
| Asn | Pro | Trp | Asn | Cys<br>305 | Asn | Cys | Asp | Ile | Leu<br>310 | Trp | Leu | Ser | Trp | Trp<br>315 |
| Ile | Lys | Asp | Met | Ala<br>320 | Pro | Ser | Asn | Thr | Ala<br>325 | Cys | Cys | Ala | Arg | Cys<br>330 |
| Asn | Thr | Pro | Pro | Asn<br>335 | Leu | Lys | Gly | Arg | Tyr<br>340 | Ile | Gly | Glu | Leu | Asp<br>345 |
| Gln | Asn | Tyr | Phe | Thr<br>350 | Cys | Tyr | Ala | Pro | Val<br>355 | Ile | Val | Glu | Pro | Pro<br>360 |
| Ala | Asp | Leu | Asn | Val<br>365 | Thr | Glu | Gly | Met | Ala<br>370 | Ala | Glu | Leu | Lys | Cys<br>375 |
| Arg | Ala | Ser | Thr | Ser<br>380 | Leu | Thr | Ser | Val | Ser<br>385 | Trp | Ile | Thr | Pro | Asn<br>390 |
| Gly | Thr | Val | Met | Thr<br>395 | His | Gly | Ala | Tyr | Lys<br>400 | Val | Arg | Ile | Ala | Val<br>405 |
| Leu | Ser | Asp | Gly | Thr<br>410 | Leu | Asn | Phe | Thr | Asn<br>415 | Val | Thr | Val | Gln | Asp<br>420 |

Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr  
 425 430 435  
 Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro  
 440 445 450  
 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser  
 455 460 465  
 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro  
 470 475 480  
 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro  
 485 490 495  
 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr  
 500 505 510  
 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr  
 515 520 525  
 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala  
 530 535 540  
 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His  
 545 550 555  
 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn  
 560 565 570  
 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu  
 575 580 585  
 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser  
 590 595 600  
 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn  
 605 610 615  
 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn  
 620 625 630  
 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile  
 635 640

&lt;210&gt; 293

&lt;211&gt; 4053

&lt;212&gt; DNA

&lt;213&gt; Homo Sapien

&lt;400&gt; 293

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[illegible]

aaa 4053

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly  
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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg  
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys  
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp  
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys  
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu  
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser  
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu  
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu  
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro  
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr  
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu  
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys  
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn





|     |     |     |     |            |     |     |     |     |     |     |     |     |     |             |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------------|
| Leu | Leu | Ile | Ile | Val<br>755 | Asp | Ser | Asp | Val | Ser | Asp | Ala | Gly | Lys | Tyr<br>765  |
| Thr | Cys | Glu | Met | Ser<br>770 | Asn | Thr | Leu | Gly | Thr | Glu | Arg | Gly | Asn | Val<br>780  |
| Arg | Leu | Ser | Val | Ile<br>785 | Pro | Thr | Pro | Thr | Cys | Asp | Ser | Pro | Gln | Met<br>795  |
| Thr | Ala | Pro | Ser | Leu<br>800 | Asp | Asp | Asp | Gly | Trp | Ala | Thr | Val | Gly | Val<br>810  |
| Val | Ile | Ile | Ala | Val<br>815 | Val | Cys | Cys | Val | Val | Gly | Thr | Ser | Leu | Val<br>825  |
| Trp | Val | Val | Ile | Ile<br>830 | Tyr | His | Thr | Arg | Arg | Arg | Asn | Glu | Asp | Cys<br>840  |
| Ser | Ile | Thr | Asn | Thr<br>845 | Asp | Glu | Thr | Asn | Leu | Pro | Ala | Asp | Ile | Pro<br>855  |
| Ser | Tyr | Leu | Ser | Ser<br>860 | Gln | Gly | Thr | Leu | Ala | Asp | Arg | Gln | Asp | Gly<br>870  |
| Tyr | Val | Ser | Ser | Glu<br>875 | Ser | Gly | Ser | His | His | Gln | Phe | Val | Thr | Ser<br>885  |
| Ser | Gly | Ala | Gly | Phe<br>890 | Phe | Leu | Pro | Gln | His | Asp | Ser | Ser | Gly | Thr<br>900  |
| Cys | His | Ile | Asp | Asn<br>905 | Ser | Ser | Glu | Ala | Asp | Val | Glu | Ala | Ala | Thr<br>915  |
| Asp | Leu | Phe | Leu | Cys<br>920 | Pro | Phe | Leu | Gly | Ser | Thr | Gly | Pro | Met | Tyr<br>930  |
| Leu | Lys | Gly | Asn | Val<br>935 | Tyr | Gly | Ser | Asp | Pro | Phe | Glu | Thr | Tyr | His<br>945  |
| Thr | Gly | Cys | Ser | Pro<br>950 | Asp | Pro | Arg | Thr | Val | Leu | Met | Asp | His | Tyr<br>960  |
| Glu | Pro | Ser | Tyr | Ile<br>965 | Lys | Lys | Lys | Glu | Cys | Tyr | Pro | Cys | Ser | His<br>975  |
| Pro | Ser | Glu | Glu | Ser<br>980 | Cys | Glu | Arg | Ser | Phe | Ser | Asn | Ile | Ser | Trp<br>990  |
| Pro | Ser | His | Val | Arg<br>995 | Lys | Leu | Leu | Asn | Thr | Ser | Tyr | Ser | His | Asn<br>1005 |
| Glu | Gly | Pro | Gly | Met        | Lys | Asn | Leu | Cys | Leu | Asn | Lys | Ser | Ser | Leu         |

| 1010  | 1015 | 1020 |
|---|------|------|
| Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn |      |      |
| 1025  | 1030 | 1035 |
| Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu |      |      |
| 1040  | 1045 | 1050 |
| Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg |      |      |
| 1055  | 1060 | 1065 |
| Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly |      |      |
| 1070  | 1075 | 1080 |
| Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn |      |      |
| 1085  | 1090 | 1095 |
| His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro |      |      |
| 1100  | 1105 | 1110 |
| Asn Phe Gln Ser Tyr Asp Leu Asp Thr                         |      |      |
| 1115  |      |      |

&lt;210&gt; 295

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 295

ggaaccgaat ctcagcta 18

&lt;210&gt; 296

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 296

cctaaactga actggacca 19

&lt;210&gt; 297

&lt;211&gt; 19

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe















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|   |     |  |     |  |     |
|---|-----|--|-----|--|-----|
|   | 425 |  | 430 |  | 435 |
| Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly |     |  |     |  |     |
|   | 440 |  | 445 |  | 450 |
| Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser |     |  |     |  |     |
|   | 455 |  | 460 |  | 465 |
| Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala |     |  |     |  |     |
|   | 470 |  | 475 |  | 480 |
| Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln |     |  |     |  |     |
|   | 485 |  | 490 |  | 495 |
| Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg     |     |  |     |  |     |
|   | 500 |  | 505 |  |     |

&lt;210&gt; 316

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 316

gatggttcct gctcaagtgc cctg 24

&lt;210&gt; 317

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 317

ttgcacttgt aggacccacg tacg 24

&lt;210&gt; 318

&lt;211&gt; 50

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 318

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&lt;210&gt; 319

&lt;211&gt; 2110

&lt;212&gt; DNA



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 ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400  
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 aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550  
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 aaaaaactat gccttctctt ttttttcaat caccagtagt atttttgaga 2000  
 agacttgtga aacttaagg aaatgactat taaagtctta tttttatttt 2050  
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 aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Trp | Leu | Lys | Val | Phe | Thr | Thr | Phe | Leu | Ser | Phe | Ala | Thr | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Ala | Cys | Ser | Gly | Leu | Lys | Val | Thr | Val | Pro | Ser | His | Thr | Val | His |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Gly | Val | Arg | Gly | Gln | Ala | Leu | Tyr | Leu | Pro | Val | His | Tyr | Gly | Phe |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| His | Thr | Pro | Ala | Ser | Asp | Ile | Gln | Ile | Ile | Trp | Leu | Phe | Glu | Arg |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |

|     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Pro | His | Thr | Met | Pro<br>65  | Lys | Tyr | Leu | Leu | Gly<br>70  | Ser | Val | Asn | Lys | Ser<br>75  |
| Val | Val | Pro | Asp | Leu<br>80  | Glu | Tyr | Gln | His | Lys<br>85  | Phe | Thr | Met | Met | Pro<br>90  |
| Pro | Asn | Ala | Ser | Leu<br>95  | Leu | Ile | Asn | Pro | Leu<br>100 | Gln | Phe | Pro | Asp | Glu<br>105 |
| Gly | Asn | Tyr | Ile | Val<br>110 | Lys | Val | Asn | Ile | Gln<br>115 | Gly | Asn | Gly | Thr | Leu<br>120 |
| Ser | Ala | Ser | Gln | Lys<br>125 | Ile | Gln | Val | Thr | Val<br>130 | Asp | Asp | Pro | Val | Thr<br>135 |
| Lys | Pro | Val | Val | Gln<br>140 | Ile | His | Pro | Pro | Ser<br>145 | Gly | Ala | Val | Glu | Tyr<br>150 |
| Val | Gly | Asn | Met | Thr<br>155 | Leu | Thr | Cys | His | Val<br>160 | Glu | Gly | Gly | Thr | Arg<br>165 |
| Leu | Ala | Tyr | Gln | Trp<br>170 | Leu | Lys | Asn | Gly | Arg<br>175 | Pro | Val | His | Thr | Ser<br>180 |
| Ser | Thr | Tyr | Ser | Phe<br>185 | Ser | Pro | Gln | Asn | Asn<br>190 | Thr | Leu | His | Ile | Ala<br>195 |
| Pro | Val | Thr | Lys | Glu<br>200 | Asp | Ile | Gly | Asn | Tyr<br>205 | Ser | Cys | Leu | Val | Arg<br>210 |
| Asn | Pro | Val | Ser | Glu<br>215 | Met | Glu | Ser | Asp | Ile<br>220 | Ile | Met | Pro | Ile | Ile<br>225 |
| Tyr | Tyr | Gly | Pro | Tyr<br>230 | Gly | Leu | Gln | Val | Asn<br>235 | Ser | Asp | Lys | Gly | Leu<br>240 |
| Lys | Val | Gly | Glu | Val<br>245 | Phe | Thr | Val | Asp | Leu<br>250 | Gly | Glu | Ala | Ile | Leu<br>255 |
| Phe | Asp | Cys | Ser | Ala<br>260 | Asp | Ser | His | Pro | Pro<br>265 | Asn | Thr | Tyr | Ser | Trp<br>270 |
| Ile | Arg | Arg | Thr | Asp<br>275 | Asn | Thr | Thr | Tyr | Ile<br>280 | Ile | Lys | His | Gly | Pro<br>285 |
| Arg | Leu | Glu | Val | Ala<br>290 | Ser | Glu | Lys | Val | Ala<br>295 | Gln | Lys | Thr | Met | Asp<br>300 |
| Tyr | Val | Cys | Cys | Ala<br>305 | Tyr | Asn | Asn | Ile | Thr<br>310 | Gly | Arg | Gln | Asp | Glu<br>315 |
| Thr | His | Phe | Thr | Val        | Ile | Ile | Thr | Ser | Val        | Gly | Leu | Glu | Lys | Leu        |

| 320 |     |     |     |     |     |     |     |     |     | 325 |     |     |     |     | 330 |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|
| Ala | Gln | Lys | Gly | Lys | Ser | Leu | Ser | Pro | Leu | Ala | Ser | Ile | Thr | Gly |     |  |  |  |  |
|     |     |     |     | 335 |     |     |     |     | 340 |     |     |     |     | 345 |     |  |  |  |  |
| Ile | Ser | Leu | Phe | Leu | Ile | Ile | Ser | Met | Cys | Leu | Leu | Phe | Leu | Trp |     |  |  |  |  |
|     |     |     |     | 350 |     |     |     |     | 355 |     |     |     |     | 360 |     |  |  |  |  |
| Lys | Lys | Tyr | Gln | Pro | Tyr | Lys | Val | Ile | Lys | Gln | Lys | Leu | Glu | Gly |     |  |  |  |  |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |     |  |  |  |  |
| Arg | Pro | Glu | Thr | Glu | Tyr | Arg | Lys | Ala | Gln | Thr | Phe | Ser | Gly | His |     |  |  |  |  |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |     |  |  |  |  |
| Glu | Asp | Ala | Leu | Asp | Asp | Phe | Gly | Ile | Tyr | Glu | Phe | Val | Ala | Phe |     |  |  |  |  |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |     |  |  |  |  |
| Pro | Asp | Val | Ser | Gly | Val | Ser | Arg | Ile | Pro | Ser | Arg | Ser | Val | Pro |     |  |  |  |  |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |     |  |  |  |  |
| Ala | Ser | Asp | Cys | Val | Ser | Gly | Gln | Asp | Leu | His | Ser | Thr | Val | Tyr |     |  |  |  |  |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |     |  |  |  |  |
| Glu | Val | Ile | Gln | His | Ile | Pro | Ala | Gln | Gln | Gln | Asp | His | Pro | Glu |     |  |  |  |  |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |     |  |  |  |  |

&lt;210&gt; 321

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 321

gatcctgtca caaagccagt ggtgc 25

&lt;210&gt; 322

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 322

cactgacagg gttcctcacc cagg 24

&lt;210&gt; 323

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence









|   |     |     |
|---|-----|-----|
| 215   | 220 | 225 |
| Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu |     |     |
| 230   | 235 | 240 |
| Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu |     |     |
| 245   | 250 | 255 |
| Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser |     |     |
| 260   | 265 | 270 |
| Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser                     |     |     |
| 275   | 280 |     |

&lt;210&gt; 326

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 326

tgaggtgggc aagcggcgaa atg 23

&lt;210&gt; 327

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 327

tatgtggatc aggacgtgcc 20

&lt;210&gt; 328

&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic Oligonucleotide Probe

&lt;400&gt; 328

tgcagggttc agtctagatt g 21

&lt;210&gt; 329

&lt;211&gt; 25

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence





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cctaccagaa aaaaaaaaa 2168

<210> 332

<211> 533

<212> PRT

<213> Homo Sapien

<400> 332

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20 25 30

Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys  
35 40 45

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser  
50 55 60

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp  
65 70 75

Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val  
80 85 90

Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu  
95 100 105

Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg  
110 115 120

Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala  
125 130 135

Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile  
140 145 150

Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser  
155 160 165

Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly  
170 175 180

Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln  
185 190 195

Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu  
200 205 210

|     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Asp | Tyr | Leu | Ser | Tyr<br>215 | Ala | Val | Phe | Gln | Leu<br>220 | Gly | Asp | Leu | His | Arg<br>225 |
| Ala | Leu | Glu | Leu | Thr<br>230 | Arg | Arg | Leu | Leu | Ser<br>235 | Leu | Asp | Pro | Ser | His<br>240 |
| Glu | Arg | Ala | Gly | Gly<br>245 | Asn | Leu | Arg | Tyr | Phe<br>250 | Glu | Gln | Leu | Leu | Glu<br>255 |
| Glu | Glu | Arg | Glu | Lys<br>260 | Thr | Leu | Thr | Asn | Gln<br>265 | Thr | Glu | Ala | Glu | Leu<br>270 |
| Ala | Thr | Pro | Glu | Gly<br>275 | Ile | Tyr | Glu | Arg | Pro<br>280 | Val | Asp | Tyr | Leu | Pro<br>285 |
| Glu | Arg | Asp | Val | Tyr<br>290 | Glu | Ser | Leu | Cys | Arg<br>295 | Gly | Glu | Gly | Val | Lys<br>300 |
| Leu | Thr | Pro | Arg | Arg<br>305 | Gln | Lys | Arg | Leu | Phe<br>310 | Cys | Arg | Tyr | His | His<br>315 |
| Gly | Asn | Arg | Ala | Pro<br>320 | Gln | Leu | Leu | Ile | Ala<br>325 | Pro | Phe | Lys | Glu | Glu<br>330 |
| Asp | Glu | Trp | Asp | Ser<br>335 | Pro | His | Ile | Val | Arg<br>340 | Tyr | Tyr | Asp | Val | Met<br>345 |
| Ser | Asp | Glu | Glu | Ile<br>350 | Glu | Arg | Ile | Lys | Glu<br>355 | Ile | Ala | Lys | Pro | Lys<br>360 |
| Leu | Ala | Arg | Ala | Thr<br>365 | Val | Arg | Asp | Pro | Lys<br>370 | Thr | Gly | Val | Leu | Thr<br>375 |
| Val | Ala | Ser | Tyr | Arg<br>380 | Val | Ser | Lys | Ser | Ser<br>385 | Trp | Leu | Glu | Glu | Asp<br>390 |
| Asp | Asp | Pro | Val | Val<br>395 | Ala | Arg | Val | Asn | Arg<br>400 | Arg | Met | Gln | His | Ile<br>405 |
| Thr | Gly | Leu | Thr | Val<br>410 | Lys | Thr | Ala | Glu | Leu<br>415 | Leu | Gln | Val | Ala | Asn<br>420 |
| Tyr | Gly | Val | Gly | Gly<br>425 | Gln | Tyr | Glu | Pro | His<br>430 | Phe | Asp | Phe | Ser | Arg<br>435 |
| Arg | Pro | Phe | Asp | Ser<br>440 | Gly | Leu | Lys | Thr | Glu<br>445 | Gly | Asn | Arg | Leu | Ala<br>450 |
| Thr | Phe | Leu | Asn | Tyr<br>455 | Met | Ser | Asp | Val | Glu<br>460 | Ala | Gly | Gly | Ala | Thr<br>465 |
| Val | Phe | Pro | Asp | Leu<br>470 | Gly | Ala | Ala | Ile | Trp<br>475 | Pro | Lys | Lys | Gly | Thr<br>480 |









tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150  
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 ccaggagttc aatcctgccc tgtcaccaca gagatcacc ccagggcccc 2250  
 cgggggctgg cctgacccc cctccctc ctggtgctga cccctcccg 2300  
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 gccgcctgg gggccctaac ctattacct ttcctttgtc tgcctcagcc 2700  
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<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Leu | Ser | Ser | Leu | Leu | Ala | Leu | Leu | Arg | Pro | Ala | Leu | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Leu | Gly | Leu | Ser | Leu | Gly | Cys | Ser | Leu | Ser | Leu | Leu | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ser | Trp | Ile | Gln | Gly | Glu | Gly | Glu | Asp | Pro | Cys | Val | Glu | Ala |
|     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gly | Glu | Arg | Gly | Gly | Pro | Gln | Asn | Pro | Asp | Ser | Arg | Ala | Arg |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Asp | Gln | Ser | Asp | Glu | Asp | Phe | Lys | Pro | Arg | Ile | Val | Pro | Tyr |
|     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Arg | Asp | Pro | Asn | Lys | Pro | Tyr | Lys | Lys | Val | Leu | Arg | Thr | Arg |
|     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ile | Gln | Thr | Glu | Leu | Gly | Ser | Arg | Glu | Arg | Leu | Leu | Val | Ala |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Pro | Phe | Thr | Pro | His | Ser | Arg | Phe | Glu | Val | Leu | Gly | Trp |
|     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     | 375 |
| Asp | Tyr | Phe | Thr | Glu | Gln | His | Thr | Phe | Ser | Cys | Ala | Asp | Gly | Ala |
|     |     |     |     | 380 |     |     |     |     | 385 |     |     |     |     | 390 |
| Pro | Lys | Cys | Pro | Leu | Gln | Gly | Ala | Ser | Arg | Ala | Asp | Val | Gly | Asp |
|     |     |     |     | 395 |     |     |     |     | 400 |     |     |     |     | 405 |
| Ala | Leu | Glu | Thr | Ala | Leu | Glu | Gln | Leu | Asn | Arg | Arg | Tyr | Gln | Pro |
|     |     |     |     | 410 |     |     |     |     | 415 |     |     |     |     | 420 |
| Arg | Leu | Arg | Phe | Gln | Lys | Gln | Arg | Leu | Leu | Asn | Gly | Tyr | Arg | Arg |
|     |     |     |     | 425 |     |     |     |     | 430 |     |     |     |     | 435 |
| Phe | Asp | Pro | Ala | Arg | Gly | Met | Glu | Tyr | Thr | Leu | Asp | Leu | Leu | Leu |
|     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |     | 450 |
| Glu | Cys | Val | Thr | Gln | Arg | Gly | His | Arg | Arg | Ala | Leu | Ala | Arg | Arg |
|     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     | 465 |
| Val | Ser | Leu | Leu | Arg | Pro | Leu | Ser | Arg | Val | Glu | Ile | Leu | Pro | Met |
|     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |     | 480 |
| Pro | Tyr | Val | Thr | Glu | Ala | Thr | Arg | Val | Gln | Leu | Val | Leu | Pro | Leu |
|     |     |     |     | 485 |     |     |     |     | 490 |     |     |     |     | 495 |
| Leu | Val | Ala | Glu | Ala | Ala | Ala | Ala | Pro | Ala | Phe | Leu | Glu | Ala | Phe |
|     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |
| Ala | Ala | Asn | Val | Leu | Glu | Pro | Arg | Glu | His | Ala | Leu | Leu | Thr | Leu |
|     |     |     |     | 515 |     |     |     |     | 520 |     |     |     |     | 525 |
| Leu | Leu | Val | Tyr | Gly | Pro | Arg | Glu | Gly | Gly | Arg | Gly | Ala | Pro | Asp |
|     |     |     |     | 530 |     |     |     |     | 535 |     |     |     |     | 540 |
| Pro | Phe | Leu | Gly | Val | Lys | Ala | Ala | Ala | Ala | Glu | Leu | Glu | Arg | Arg |
|     |     |     |     | 545 |     |     |     |     | 550 |     |     |     |     | 555 |
| Tyr | Pro | Gly | Thr | Arg | Leu | Ala | Trp | Leu | Ala | Val | Arg | Ala | Glu | Ala |
|     |     |     |     | 560 |     |     |     |     | 565 |     |     |     |     | 570 |
| Pro | Ser | Gln | Val | Arg | Leu | Met | Asp | Val | Val | Ser | Lys | Lys | His | Pro |
|     |     |     |     | 575 |     |     |     |     | 580 |     |     |     |     | 585 |
| Val | Asp | Thr | Leu | Phe | Phe | Leu | Thr | Thr | Val | Trp | Thr | Arg | Pro | Gly |
|     |     |     |     | 590 |     |     |     |     | 595 |     |     |     |     | 600 |
| Pro | Glu | Val | Leu | Asn | Arg | Cys | Arg | Met | Asn | Ala | Ile | Ser | Gly | Trp |
|     |     |     |     | 605 |     |     |     |     | 610 |     |     |     |     | 615 |
| Gln | Ala | Phe | Phe | Pro | Val | His | Phe | Gln | Glu | Phe | Asn | Pro | Ala | Leu |
|     |     |     |     | 620 |     |     |     |     | 625 |     |     |     |     | 630 |

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp  
 635 640 645  
 Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile  
 650 655 660  
 Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr  
 665 670 675  
 Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu  
 680 685 690  
 Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met  
 695 700 705  
 Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val  
 710 715 720  
 Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro  
 725 730 735  
 Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu  
 740 745 750  
 Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu  
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 Gln Glu Gln Ala Asn Ser Thr  
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<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

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 ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150  
 tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200  
 catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250  
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 accaaacact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400

00004330 074304

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 aagcttaciaa atacgccttt gataagtata gagaccaata caactgggtc 500  
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<210> 341

<211> 318

<212> PRT

<213> Homo Sapien

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Ser | Glu | Ser | Ser | Ser | Phe | Leu | Lys | Gly | Val | Met | Leu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Ser | Ile | Phe | Cys | Ala | Leu | Ile | Thr | Met | Leu | Gly | His | Ile | Arg | Ile |
|     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Gly | His | Gly | Asn | Arg | Met | His | His | His | Glu | His | His | His | Leu | Gln |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Ala | Pro | Asn | Lys | Glu | Asp | Ile | Leu | Lys | Ile | Ser | Glu | Asp | Glu | Arg |
|     |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Met | Glu | Leu | Ser | Lys | Ser | Phe | Arg | Val | Tyr | Cys | Ile | Ile | Leu | Val |
|     |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Lys | Pro | Lys | Asp | Val | Ser | Leu | Trp | Ala | Ala | Val | Lys | Glu | Thr | Trp |
|     |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Thr | Lys | His | Cys | Asp | Lys | Ala | Glu | Phe | Phe | Ser | Ser | Glu | Asn | Val |
|     |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Lys | Val | Phe | Glu | Ser | Ile | Asn | Met | Asp | Thr | Asn | Asp | Met | Trp | Leu |
|     |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Met | Met | Arg | Lys | Ala | Tyr | Lys | Tyr | Ala | Phe | Asp | Lys | Tyr | Arg | Asp |
|     |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Gln | Tyr | Asn | Trp | Phe | Phe | Leu | Ala | Arg | Pro | Thr | Thr | Phe | Ala | Ile |
|     |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Ile | Glu | Asn | Leu | Lys | Tyr | Phe | Leu | Leu | Lys | Lys | Asp | Pro | Ser | Gln |
|     |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |
| Pro | Phe | Tyr | Leu | Gly | His | Thr | Ile | Lys | Ser | Gly | Asp | Leu | Glu | Tyr |
|     |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |
| Val | Gly | Met | Glu | Gly | Gly | Ile | Val | Leu | Ser | Val | Glu | Ser | Met | Lys |
|     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |
| Arg | Leu | Asn | Ser | Leu | Leu | Asn | Ile | Pro | Glu | Lys | Cys | Pro | Glu | Gln |
|     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     | 210 |
| Gly | Gly | Met | Ile | Trp | Lys | Ile | Ser | Glu | Asp | Lys | Gln | Leu | Ala | Val |
|     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     | 225 |
| Cys | Leu | Lys | Tyr | Ala | Gly | Val | Phe | Ala | Glu | Asn | Ala | Glu | Asp | Ala |
|     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Asp | Gly | Lys | Asp | Val | Phe | Asn | Thr | Lys | Ser | Val | Gly | Leu | Ser | Ile |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |
| Lys | Glu | Ala | Met | Thr | Tyr | His | Pro | Asn | Gln | Val | Val | Glu | Gly | Cys |



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|---------------------|---|--|-----|--|-----|
|                     | 260   |  | 265 |  | 270 |
| Cys Ser Asp Met     | Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln |  |     |  |     |
|                     | 275   |  | 280 |  | 285 |
| Met His Val Met     | Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly |  |     |  |     |
|                     | 290   |  | 295 |  | 300 |
| His Ile Phe Asn Asp | Ala Leu Val Phe Leu Pro Pro Asn Gly Ser     |  |     |  |     |
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tgtttctctt cccaaatggt cttatggact gttgctggga tccccatcct 200

attttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250

ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300

ctctcctgct acaattatgg atcagggttca gtcaagaatt gttgtccatt 350

gaactgggaa tatttttcaat ccagctgcta cttcttttct actgacacca 400

tttctctggc gttaagttaa aagaactgct cagccatggg ggctcacctg 450

gtgggttatca actcacagga ggagcaggaa ttcctttcct acaagaaacc 500

taaaatgaga gagtttttta ttggactgtc agaccagggt gtcgaggggtc 550

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| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Cys       | Phe | Ser | Ser | Gln | Met | Phe | Leu | Trp | Thr | Val | Ala | Gly | Ile | Pro |
|           |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Ile       | Leu | Phe | Leu | Ser | Ala | Cys | Phe | Ile | Thr | Arg | Cys | Val | Val | Thr |
|           |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Phe       | Arg | Ile | Phe | Gln | Thr | Cys | Asp | Glu | Lys | Lys | Phe | Gln | Leu | Pro |
|           |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Glu       | Asn | Phe | Thr | Glu | Leu | Ser | Cys | Tyr | Asn | Tyr | Gly | Ser | Gly | Ser |
|           |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Val       | Lys | Asn | Cys | Cys | Pro | Leu | Asn | Trp | Glu | Tyr | Phe | Gln | Ser | Ser |
|           |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Cys       | Tyr | Phe | Phe | Ser | Thr | Asp | Thr | Ile | Ser | Trp | Ala | Leu | Ser | Leu |
|           |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Lys       | Asn | Cys | Ser | Ala | Met | Gly | Ala | His | Leu | Val | Val | Ile | Asn | Ser |
|           |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Gln       | Glu | Glu | Gln | Glu | Phe | Leu | Ser | Tyr | Lys | Lys | Pro | Lys | Met | Arg |
|           |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Glu       | Phe | Phe | Ile | Gly | Leu | Ser | Asp | Gln | Val | Val | Glu | Gly | Gln | Trp |
|           |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Gln       | Trp | Val | Asp | Gly | Thr | Pro | Leu | Thr | Lys | Ser | Leu | Ser | Phe | Trp |
|           |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |
| Asp       | Val | Gly | Glu | Pro | Asn | Asn | Ile | Ala | Thr | Leu | Glu | Asp | Cys | Ala |
|           |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val  
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Asn Pro Leu Asn Lys Gly Lys Ser Leu  
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gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300
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ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

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[illegible]

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|------------|------------|------------|-------------|-------------|------|
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| gcctcttcct | gagatgacta | ggacagtctg | tacccagagg  | ccaccagaa   | 2150 |
| gccctcagat | gtacatacac | agatgccagt | cagctcctgg  | ggttgcgcca  | 2200 |
| ggcgcccccg | ctctagctca | ctgttgccct | gctgtctgcc  | aggaggccct  | 2250 |
| gccatccttg | ggccctggca | gtggctgtgt | cccagtgagc  | ttactcacg   | 2300 |
| tggcccttgc | ttcatccagc | acagctctca | ggtgggcact  | gcagggacac  | 2350 |
| tggtgtcttc | catgtagcgt | cccagctttg | ggctcctgta  | acagacctct  | 2400 |
| ttttggttat | ggatggctca | caaaataggg | ccccaatgc   | tatTTTTTTT  | 2450 |
| ttttaagttt | gtttaattat | ttgttaagat | tgtctaaggc  | caaaggcaat  | 2500 |
| tgcgaaatca | agtctgtcaa | gtacaataac | atTTTTTaaa  | gaaatggat   | 2550 |
| cccactgttc | ctctttgcca | cagagaaagc | accagacgc   | cacaggctct  | 2600 |
| gtcgcatttc | aaaacaaacc | atgatggagt | ggcggccagt  | ccagcctttt  | 2650 |
| aaagaacgtc | aggtggagca | gccaggtgaa | aggcctggcg  | gggaggaaag  | 2700 |
| tgaaacgcct | gaatcaaaag | cagttttcta | atTTTtgactt | taaatTTTTt  | 2750 |
| atccgccgga | gacactgctc | ccatttgtgg | ggggacatta  | gcaacatcac  | 2800 |
| tcagaagcct | gtgttcttca | agagcaggtg | ttctcagcct  | cacatgccct  | 2850 |
| gccgtgctgg | actcaggact | gaagtgctgt | aaagcaagga  | gctgctgaga  | 2900 |
| aggagcactc | cactgtgtgc | ctggagaatg | gctctcacta  | ctcaccttgt  | 2950 |
| ctttcagctt | ccagtgtctt | gggtTTTTta | tactttgaca  | gctTTTTTTT  | 3000 |
| aattgcatac | atgagactgt | gttgactttt | tttagttatg  | tgaaacactt  | 3050 |
| tgccgcaggc | cgctggcag  | aggcaggaaa | tgctccagca  | gtggctcagt  | 3100 |
| gtccctgggt | gtctgctgca | tggcatcctg | gatgcttagc  | atgcaagttc  | 3150 |
| cctccatcat | tgccaccttg | gtagagaggg | atggctcccc  | accctcagcg  | 3200 |
| ttggggattc | acgctccagc | ctccttcttg | gttgctcatag | tgatagggta  | 3250 |
| gccttattgc | cccctcttct | tataccctaa | aaccttctac  | actagtgccca | 3300 |
| tgggaaccag | gtctgaaaaa | gtagagagaa | gtgaaagtag  | agtctgggaa  | 3350 |
| gtagctgcct | ataactgaga | ctagacggaa | aaggaatact  | cgtgtatttt  | 3400 |

[illegible]

|           |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| <400> 423 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| Met       | Ala | Leu | Arg | Arg | Pro | Pro | Arg | Leu | Arg | Leu | Cys | Ala | Arg | Leu |
| 1         |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |
| Pro       | Asp | Phe | Phe | Leu | Leu | Leu | Leu | Phe | Arg | Gly | Cys | Leu | Ile | Gly |
|           |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |
| Ala       | Val | Asn | Leu | Lys | Ser | Ser | Asn | Arg | Thr | Pro | Val | Val | Gln | Glu |
|           |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |
| Phe       | Glu | Ser | Val | Glu | Leu | Ser | Cys | Ile | Ile | Thr | Asp | Ser | Gln | Thr |
|           |     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |
| Ser       | Asp | Pro | Arg | Ile | Glu | Trp | Lys | Lys | Ile | Gln | Asp | Glu | Gln | Thr |
|           |     |     |     | 65  |     |     |     |     | 70  |     |     |     |     | 75  |
| Thr       | Tyr | Val | Phe | Phe | Asp | Asn | Lys | Ile | Gln | Gly | Asp | Leu | Ala | Gly |
|           |     |     |     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |
| Arg       | Ala | Glu | Ile | Leu | Gly | Lys | Thr | Ser | Leu | Lys | Ile | Trp | Asn | Val |
|           |     |     |     | 95  |     |     |     |     | 100 |     |     |     |     | 105 |
| Thr       | Arg | Arg | Asp | Ser | Ala | Leu | Tyr | Arg | Cys | Glu | Val | Val | Ala | Arg |
|           |     |     |     | 110 |     |     |     |     | 115 |     |     |     |     | 120 |
| Asn       | Asp | Arg | Lys | Glu | Ile | Asp | Glu | Ile | Val | Ile | Glu | Leu | Thr | Val |
|           |     |     |     | 125 |     |     |     |     | 130 |     |     |     |     | 135 |
| Gln       | Val | Lys | Pro | Val | Thr | Pro | Val | Cys | Arg | Val | Pro | Lys | Ala | Val |
|           |     |     |     | 140 |     |     |     |     | 145 |     |     |     |     | 150 |
| Pro       | Val | Gly | Lys | Met | Ala | Thr | Leu | His | Cys | Gln | Glu | Ser | Glu | Gly |
|           |     |     |     | 155 |     |     |     |     | 160 |     |     |     |     | 165 |
| His       | Pro | Arg | Pro | His | Tyr | Ser | Trp | Tyr | Arg | Asn | Asp | Val | Pro | Leu |
|           |     |     |     | 170 |     |     |     |     | 175 |     |     |     |     | 180 |
| Pro       | Thr | Asp | Ser | Arg | Ala | Asn | Pro | Arg | Phe | Arg | Asn | Ser | Ser | Phe |
|           |     |     |     | 185 |     |     |     |     | 190 |     |     |     |     | 195 |

| Year | 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| 1990 | 1991 | 1992 | 1993 | 1994 | 1995 | 1996 | 1997 | 1998 | 1999 | 2000 | 2001 | 2002 | 2003 | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | 2018 | 2019 | 2020 | 2021 | 2022 | 2023 | 2024 | 2025 | 2026 | 2027 | 2028 | 2029 | 2030 | 2031 | 2032 | 2033 | 2034 | 2035 | 2036 | 2037 | 2038 | 2039 | 2040 | 2041 | 2042 | 2043 | 2044 | 2045 | 2046 | 2047 | 2048 | 2049 | 2050 | 2051 | 2052 | 2053 | 2054 | 2055 | 2056 | 2057 | 2058 | 2059 | 2060 | 2061 | 2062 | 2063 | 2064 | 2065 | 2066 | 2067 | 2068 | 2069 | 2070 | 2071 | 2072 | 2073 | 2074 | 2075 | 2076 | 2077 | 2078 | 2079 | 2080 | 2081 | 2082 | 2083 | 2084 | 2085 | 2086 | 2087 | 2088 | 2089 | 2090 | 2091 | 2092 | 2093 | 2094 | 2095 | 2096 | 2097 | 2098 | 2099 | 2100 |      |